

2 32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG
arg val asn arg ser arg ser leu ser asn ser asn pro asp ile ser gly thr pro thr

62 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC
ser pro asp asp glu val arg ser ile ile gly ser lys gly leu asp arg ser asn ser

122 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA
trp val asn thr gly gly pro lys ala ala pro trp gly ser asn pro ser pro ser ala

182 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
glu ser thr gln ala met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332
GGT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp

362 392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

Cadherin

422 |xxx cleavage xx| 452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro

1382
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1412
1442
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1472
1502
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu

1532
1562
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1592
1622
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu

1652
1682
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1712
1742
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1772
1802
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn

1832
1862
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1892
1922
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1952
1982
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2012
2042
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2072

2102 2132
 ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
 met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192
 TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
 ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252
 CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
 pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312
 ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
 met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372
 ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
 gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 |xxxxxxxxxxxxxxxxxxxx transmembrane domain xxxxxxxxxxxxxxxxxxxxxxx
 TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
 ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val
 |xxxxxxxxxxxxxxxxxxxx|

2492
 GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
 ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

2522 2552
 CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
 gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612
 GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
 asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672 |xxxxx ITAM xxxx| |xxx
 GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
 glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr
 xx ITAM xxx|

2732
 AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
 lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his

2762 2792
 GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
 gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 |xxxxx ITAM xxxx| 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu

2942 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032 |xxxxx ITAM xxxx|
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr

3242 3272 |xxxxxxxxxxxxxxxxxxxxxxxxxxxx|
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

xxxxxxxxxxxxxxxxxxxxxxxxxxxxx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

xxxxxxxxxxxxxxxxxxxxxxxxxxxxx| 3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422 3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482 3512 |xxxxxxxxxxxxx|
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

XXXXXXXXXXXXXXXXXXXXX Coiled coil 2 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX|

AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602

3632

TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro STP

3662

3692

TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722

3752

TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782

3812

TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842

3872

AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902

3932

GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962

3992

CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022

4052

TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG

4082

4112

TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142

CTC

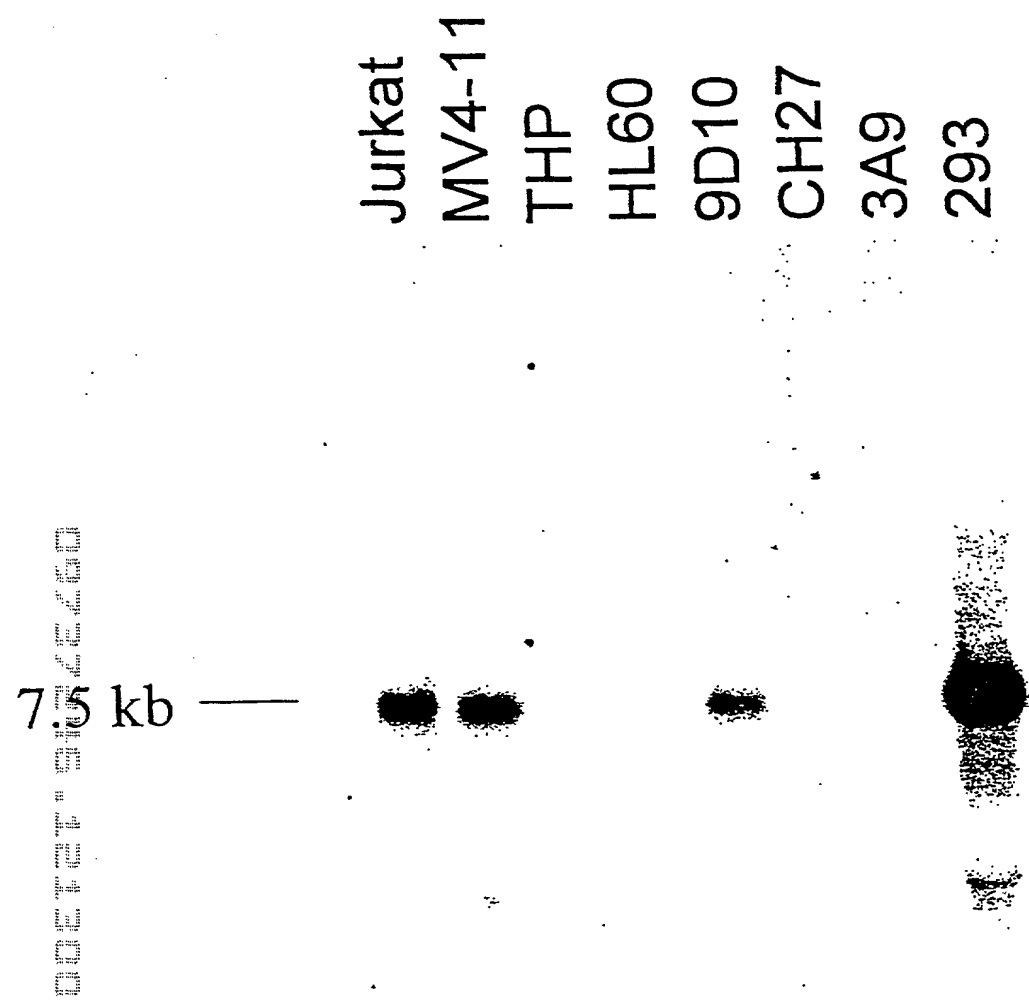
546 →

PBL
lung
placenta
sm intestine
liver
kidney
spleen
thymus
colon
skel muscle
heart
brain



A

Human CLASP-3 Multiple Cell Lines Northern



HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPEFYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGVFTRSAFAAVLHHHQNPEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLNFFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSISLISNSARV
HC5	-----
HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMIAFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

HC2A	I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
KIAA	I IHVVAQCHEEGLESHLRSYVKYAYKAEPYVASEYKTVHEELTKSMTTILKPSADFLTSN
rat	-----
HC4	LFHIVSKCHEEGLDSYLSSFIKYSFRPGKPSAPQAPLIHETLATMMIALLKQSADFLAIN
HC1	LPDIVAKCHEEQLDHSVQSYIKFVFKTR---ACKERPVEDDLAKNVTGLLK-SNDSPTVK
HC3	TQAMDRSCNRMSSHTETSSFLQTLTGRLP----TKKLFHEELALQWVVCSSG---SVR---E
HC5	-----

Cadherin

Cleavage

HC2A	KLLRYSWFFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFFDVLIKSMAQHLENSKVKLIRNORFPASYHHAVETVVNMLMPHITQKFRD
rat	-----
HC4	KLLKYSWFFFEIIAKSMATYLLLEENKIKLTHGQRFKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFFAIILKSMAQHLEIDTNKIQLHRPQRFPESYQNELDNLVMSVLSDHVIWKYKD
HC3	SALQQAFFFELMVKSMVHHLYFNDKLEARRKSRFPERFMDIAALVSTIASDIVSRFQK
HC5	-----

HC2A	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
KIAA	NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN---NYIS--CFAPGDPKTLFEYKFEFL
rat	-----
HC4	IPKESRNVNYSIASFLKCCLTIMDRGFVFNLIN---DYIS--GFSPKDPKVLAEYKFEFL
HC1	ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN---NYIS--MFSSGDLKTLQCQYKFDL
HC3	DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYQVSSKLYSLPNPSVLVSLRLDFL
HC5	-----

HC2A	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
KIAA	RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL----DYSLTDEF
rat	-----
HC4	QTICNHEHYIPLNLPM-----AFAKPKLQR-----VQDSNL----EYSLSDEY
HC1	QEVQCQEHFIPLCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3	RIICSHEHYVTNLNPLCSLLTPPASPSVSSATSQSSGFSTNVQDQKIANMFELS--VPF
HC5	-----MNADTAPTSPCPSIS---SQNSSSCSSFDQKIASMFDRTSRVPA

Cadherin

EC motif

HC2A	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA	CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat	-----
HC4	CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNLLIKHAFDTRYQHKNQQAQIAQ
HC1	CRKHFLIGILLREVG FALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3	ROOHYLAGIVLTELAVILDPDAEGLFGLHKKVINMVHNLSSHSDPRYSDPQIKARVAM
HC5	SSTS-SPGILFTELAAALDAEGEGISEVQRKAVSAIHSLLSSHDLDPRCVKPEVKVKIAA

HC2A	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
KIAA	LYLPLFGLLIENVQRINVRDVSPFPVNAG-MTVKDESLALPAVNPLVTPQKGSTLDNSLH
rat	-----
HC4	LYLPLFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSLS
HC1	LYMPLYGMLLDNMPRIYLDLYPFTVNTSNQGSRDDLTNGGFQSQTAKHANSVDTSFS
HC3	LYLPLIGIIMETVPQLYDFETETHNQRGRPICIAATDDYESE-----SG---SMIS
HC5	LYLPLVGIILDALPQLCDFTVADTRRYR---TSGSDEEQE-----GA---GAIT

HC2A KDLGAIISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 KIAA' KDLGAIISGIASPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 rat -----
 HC4 TDKDTAYGSFQNG-----HGIKREDSRGS LIP-EGATGFPDQGN TGEN-----TRQS
 HC1 KDVLSNIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPL
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLIMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLIMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLIMCYLYIVKMISED TLLTYWN-KVSPQELINILILEVCL
 HC1 ALIGSTLRFDRLDQAE TRSLIMCF LHMKTISYETLIAYWQ-RAPSPEVSDFFSILDVCL
 HC3 -----TFSAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLCV
 HC5 -----MLNADTTRNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFQYM GKRYIARNQEGLG--PIVHDRKS-----QTLFVSRNRTGMM
 KIAA HQFQYM GKRYIAR-----TGM
 rat -----
 HC4 FHFRYM GKRN IARVHDAWLSKHFGIDRKS-----QTMPALNRNSGVM
 HC1 QNFRYL GKRN IIRKIAAAF--KFVQSTQNNGT LKGSNPSCQTSGLLAQWMHSTSRHEGHK
 HC3 SCFEYK GKKVFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
 HC5 LCFEYK GKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGE GARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADI FHQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK---NALS NPKL----LQMLDNTMTS NSNEIDIVHHVDTEAN IATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWRKDMTHWRQNT EKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 KIAA LTALDTLSLFTLAFKNQLLADHGHNP LMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIY
 rat -----
 HC4 -----KLSRGHSP LMKKVFDVYLCFLQKHQSE MALKNVFTALRS LIY
 HC1 LTVLDTISFFTQCFKTHFLNNDGHNP LMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC3 LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQV NQSATALKHVFASLRLFVC
 HC5 LIILD TLEIVVQTVS--VTES--KESILGGVLKVLHSMACNQSAVYLQHC FATQRALVS
 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNC DQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYT GKKS FVRTH
 HC4 KFPSAFFKGRVNMCAAF CYEVLKCC TSKISS TRNEASALLYLLMRNNFEYTKRKTFLRTH
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSH
 HC3 KFPELLFEEETEQCADLCRLLRHCSSSIGTIRSHPSASLYLLMRQNF EIGN--N FARVK
 HC5 KFGDLLFEEVEQC FDLCHQVLHHCSSSMDVTRS QACATLYLLMRFSFGATS--N FARVK

HC2A LQV IISVSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 KIAA LQV IISVSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 rat LQV IISLSQ LIADVVGIGETR FQQSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLM
 HC4 LQIIIAVSQ LIADVALSGGSRFQESLFI INNFANS DRPMLARAFPAEVKDLTKRIRTVLM
 HC1 LQLIKAVSQ LIAD-AGIGGSRFQHS LAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLM
 HC3 MQVPMSLSSLVGTSQNFNEEFLRRSLKTI LTYAEEDLELRETTFPDQVQDLVFNLMILS
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTI LAYSEEDTAMQMPPTQVEELLCNLNSILY

Coiled-Coil 1

HC2A	IHCFFPVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
KIAA	IHCFFPVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELRQLCSSAEVDMIKLQLKLQGSV
rat	IHCFFPVKKRIPVMYQHHTDLNFI	IEVAIDEMSKKVAELHQLCSSAEVDMIKLQLKLQGSV
HC4	SNSFFPVKKRIPINCEQQINLKF	IDGATDEIKDKTAELOKLCSSSTDVDMIQQLKLQGWV
HC1	SHLFFPVKKRIQVISQSSTELNFI	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV
HC3	SHAFFYIKTRVNVTHKEEIIILTR	IEVAIEDMQKKTQELAFATHQDPADPKMLQMVLCQSV
HC5	MHAFFYIKTRISVIQKEEFVLTR	IEVAIEDMKKKTLQLAVAINQEPDAKMLQMVLCQSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
rat	SVQVNAGPLAYARAFLLDDTNTKRYPDNKVKLLKEVFRQFVEACGQAL	LAVNERLIKEDQLE
HC4	SVQVNAGPLAYARAFLLNDSQASKYPPKKVSELKDMFRKFIQACSI	LELNERLIKEDQVE
HC1	SVKVNAGPMAYARAFLEETNAKKYPDNQVKLLKEIFRQFADACGQAL	LDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQVFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDAL	RKNKSLIGPVQKE
HC5	GATVNQGPLEVAQVFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

Coiled-Coil 2

HC2A	YQEEMKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTPPTSTMVHGMTSS
KIAA	YQEEMKANYREMAKELSEIMHE	QLG-----
rat	YQEEMKANYREIRKELSDIIVER	ICPGEDKRA TKFPAHLQRHQRTDNKHSGSRVDQFILS
HC4	YHEGLKSNFRDMVKELSDIIEH	QILQEDTMHSPWMSNTLHVFCALSGTSSDRGYGSPRYA
HC1	YQEELRSHYKMLSELSTVMNEQ	ITGRDDLK---RGVDQTCTRVISKATPALPTVSISS
HC3	YQRELG---KLSS---	PZ-----
HC5	YQELKKNYNKLKENLRPMIERK	IPELYKPIFRVESQKRDSFHRSSFRKCETQLSQGSZ-

PBM

HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPHEPHVGTCTFVMCKLRTTFRANHWFCQAQEEAMNGGREKEPWTVIFNSRFYRSWGK
HC4	EVZ-----
HC1	SAEVZ-----
HC3	-----
HC5	-----

HC2A	----
KIAA	----
rat	VHIFF
HC4	----
HC1	----
HC3	----
HC5	----

2 32
CGA GTA AAT CGT TCT CGA AGC CTT AGT AAT AGC AAT CCA GAT ATA TCT GGG ACT CCC ACG

62 92
TCA CCA GAT GAT GAA GTT CGA TCA ATC ATC GGG AGT AAG GGT TTA GAT CGC TCC AAT TCC

122 152
TGG GTT AAC ACT GGT GGT CCA AAA GCT GCC CCA TGG GGA TCC AAC CCC AGT CCA AGT GCA

182 212
GAA TCA ACA CAG GCT ATG GAT CGA AGT TGT AAT CGT ATG TCT TCG CAC ACA GAG ACG TCA
met asp arg ser cys asn arg met ser ser his thr glu thr ser

242 272
AGT TTC TTA CAA ACA TTA ACG GGA CGC TTA CCA ACT AAA AAG CTT TTT CAC GAG GAG CTG
ser phe leu gln thr leu thr gly arg leu pro thr lys lys leu phe his glu glu leu

302 332
GCT TTG CAG TGG GTT GTT TGC AGT GGC AGC GTT CGG GAA TCA GCT TTG CAA CAA GCC TGG
ala leu gln trp val val cys ser gly ser val arg glu ser ala leu gln gln ala trp
ref 1.1 and 1.2
ref 2.1 and 2.2 ↓

362 392
TTC TTT TTT GAA TTA ATG GTA AAG AGC ATG GTG CAC CAT TTA TAC TTT AAT GAT AAA CTT
phe phe phe glu leu met val lys ser met val his his leu tyr phe asn asp lys leu

421 452
GAG GCT CCA AGG AAA AGT CGT TTT CCA GAA CGT TTC ATG GAT GAC ATT GCA GCT CTT GTC
glu ala pro arg lys ser arg phe pro glu arg phe met asp asp ile ala ala leu val

482 512
AGC ACG ATT GCT AGT GAT ATA GTT TCA CGA TTT CAG AAG GAC ACA GAA ATG GTT GAG AGA
ser thr ile ala ser asp ile val ser arg phe gln lys asp thr glu met val glu arg

542 572
CTC AAT ACA AGC CTT GCA TTC TTT CTC AAT GAT CTG TTG TCT GTT ATG GAC AGA GGA TTT
leu asn thr ser leu ala phe phe leu asn asp leu leu ser val met asp arg gly phe

602 632
GTT TTT AGC CTT ATA AAG TCC TGC TAT AAA CAG GTG TCT TCA AAG CTT TAC TCA TTA CCG
val phe ser leu ile lys ser cys tyr lys gln val ser ser lys leu tyr ser leu pro
ref 3.1 and 3.2 ↓

662 692
AAT CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT TTT CTA CGA ATC ATC TGC AGT CAT GAG
asn pro ser val leu val ser leu arg leu asp phe leu arg ile ile cys ser his glu

722 752
CAC TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA CTT ACT CCA CCT GCA TCT CCA TCA CCT
his tyr val thr leu asn leu pro cys ser leu leu thr pro pro ala ser pro ser pro
ref 4.1 and 4.2 ↓

782 812
TCT GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA TTT TCT ACG AAT GTA CAA GAC CAA AAG
ser val ser ser ala thr ser gln ser ser gly phe ser thr asn val gln asp gln lys

842 872
ATT GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC CGC CAA CAG CAT TAT TTG GCA GGA CTT
ile ala asn met phe glu leu ser val pro phe arg gln gln his tyr leu ala gly leu

902 932
GTG TTA ACA GAG CTG GCT GTC ATT TTA gac cct gat gct gaa gga ctg TTT GGA TTG CAT
val leu thr glu leu ala val ile leu asp pro asp ala glu gly leu phe gly leu his

962 992
AAG AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC TCC AGT CAC GAC TCA GAC CCG CGG TAC
lys lys val ile asn met val his asn leu leu ser ser his asp ser asp pro arg tyr

1022 1052
TCT GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG TTG TAT CTA CCT CTG ATT GGT ATT ATC
ser asp pro gln ile lys ala arg val ala met leu tyr leu pro leu ile gly ile ile

1082 1112
ATG GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA GAA ACT CAC AAT CAA CGA GGA AGA CCA
met glu thr val pro gln leu tyr asp phe thr glu thr his asn gln arg gly arg pro

1142 1172
ATT TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG AGC GGA AGT ATG ATA AGC CAG ACC GTT
ile cys ile ala thr asp asp tyr glu ser glu ser gly ser met ile ser gln thr val

1202 1232
GCC ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA CTA ACA AGG CCT GGC AGT TTC CTC CTC
ala met ala ile ala gly thr ser val pro gln leu thr arg pro gly ser phe leu leu
↓ ref5.1 and 5.2

1262 1292
ACG TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT TCA GCA GAA TCA AGT CGA AGC CTT TTG
thr ser thr ser gly arg gln his thr thr phe ser ala glu ser ser arg ser leu leu

1322 1352
ATC TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT GAA ACA GTT CTA CAG AAG TGG TTT ACA
ile cys leu leu trp val leu lys asn ala asp glu thr val leu gln lys trp phe thr

1382 1412
GAT CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA GAT CTG CTT TAT CTC TGT GTG TCT TGC
asp leu ser val leu gln leu asn arg leu leu asp leu leu tyr leu cys val ser cys

1442 1472
TTT GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA ATG AAT AGC TTG ACC TTT AAG AAA TCA
phe glu tyr lys gly lys lys val phe glu arg met asn ser leu thr phe lys lys ser

1502 1532
AAA GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT CTT GGG AGC ATA GGT GCC AGG CAA GAA
lys asp met arg ala lys leu glu glu ala ile leu gly ser ile gly ala arg gln glu
↓ ref 6.1 and 6.2

1562 1592
ATG GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA AGC CCA TCT GGA AGT GCC TTT GGA AGT
met val arg arg ser arg gly gln leu glu arg ser pro ser gly ser ala phe gly ser

1622 1652
CAA GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT CAC TGG CGT CAA AAC ACA GAG AAG CTT
gln glu asn leu arg trp arg lys asp met thr his trp arg gln asn thr glu lys leu

1682 1712
GAC AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA CTG ATT GAT GGA AAC CTG GCT ACA GAA
asp lys ser arg ala glu ile glu his glu ala leu ile asp gly asn leu ala thr glu

1742 1772
GCA AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT GTT GTT CAG ACC GTT TCT GTA ACG GAA
ala asn leu ile ile leu asp thr leu glu ile val val gln thr val ser val thr glu

1802 1832
TCC AAA GAG AGC ATT CTT GGT GGA GTG CTA AAA GTG CTA CTA CAC AGC ATG GCC TGT AAC
ser lys glu ser ile leu gly gly val leu lys val leu leu his ser met ala cys asn
ref 7.1 and 7.2

1862 1892
CAA AGT GCA GTT TAT CTA CAA CAC TGT TTT GCT ACA CAG AGA GCC TTG GTT TCA AAG TTT
gln ser ala val tyr leu gln his cys phe ala thr gln arg ala leu val ser lys phe

1922 1952
CCT GAA CTC TTA TTT GAA GAA GAG ACA GAG CAG TGT GCT GAT TTA TGC CTC AGG CTT CTC
pro glu leu leu phe glu glu glu thr glu gln cys ala asp leu cys leu arg leu leu

1982 2012
CGA CAC TGT AGC AGT AGC ATC GGT ACA ATA CGG TCA CAC CCC AGT GCC TCC CTT TAC CTA
arg his cys ser ser ser ile gly thr ile arg ser his pro ser ala ser leu tyr leu

2042 2072
CTA ATG AGG CAA AAC TTT GAG ATT GGG AAT AAC TTT GCC AGG GTT AAA ATG CAG GTA CCA
leu met arg gln asn phe glu ile gly asn asn phe ala arg val lys met gln val pro

2102 2132
ATG TCA CTA TCC TCC TTG GTG GGC ACA TCT CAG AAT TTT AAT GAA GAA TTC TTA AGA CGT
met ser leu ser ser leu val gly thr ser gln asn phe asn glu glu phe leu arg arg

2162 2192
TCT CTA AAG ACT ATA TTG ACA TAT GCT GAA GAA GAT CTG GAA TTG AGG GAA ACA ACA TTT
ser leu lys thr ile leu thr tyr ala glu glu asp leu glu leu arg glu thr thr phe

2222 2252
CCT GAT CAG GTC CAG GAT CTG GTT TTC AAT CTC CAT ATG ATT CTT TCT GAT ACT GTG AAA
pro asp gln val gln asp leu val phe asn leu his met ile leu ser asp thr val lys

2282 2312
ATG AAG GAA CAC CAG GAG GAT CCT GAA ATG TTG ATT GAT CTA ATG tac aga att gcc aag
met lys glu his gln glu asp pro glu met leu ile asp leu met tyr arg ile ala lys

2342 2372
ggt tac CAG ACC TCT CCA GAT CTG CGA TTG ACC TGG TTG CAG AAC ATG GCA GGC AAG CAC
gly tyr gln thr ser pro asp leu arg leu thr trp leu gln asn met ala gly lys his

2402 2432
TCA GAA CGA AGC AAT CAT GCT GAA GCT GCA CAG TGT CTA GTC CAC TCA GCA GCA CTT GTT
ser glu arg ser asn his ala glu ala ala gln cys leu val his ser ala ala leu val

2462 2492
GCT GAA TAT TTG AGC ATG CTG GAG GAC CGG AAA TAT CTT CCT GTG GGA TGT GTA ACA TTT
ala glu tyr leu ser met leu glu asp arg lys tyr leu pro val gly cys val thr phe

↓ ref 8.1 and 8.2

2552
CAG AAT ATT TCA TCT AAT GTT TTA GAA GAA TCT GCG GTC TCA GAT GAT GTG GTA TCT CCA
gln asn ile ser ser asn val leu glu glu ser ala val ser asp asp val val ser pro

2582 2612
GAT GAA GAA GGT ATC TGC TCT GGA AAA TAC TTT ACT GAG TCA GGA CTT GTG GGA TTA CTG
asp glu glu gly ile cys ser gly lys tyr phe thr glu ser gly leu val gly leu leu

2642 2672
GAA CAA GCA GCT GCT TCC TTC TCT ATG GCT GGC ATG TAT GAA GCA GTT AAT GAA GTT TAC
glu gln ala ala ala ser phe ser met ala gly met tyr glu ala val asn glu val tyr

2702 2732
AAA GTA CTT ATT CCT ATT CAT GAA GCT AAT CGG GAT GCA AAG AAA CTA TCC ACA ATT CAT
lys val leu ile pro ile his glu ala asn arg asp ala lys lys leu ser thr ile his
↓ ref 9.1

2762 2792
GGT AAA CTT CAA GAA GCA TTC AGC AAA ATT GTT CAT CAG AGT ACT GGC TGG GAG CGG ATG
gly lys leu gln glu ala phe ser lys ile val his gln ser thr gly trp glu arg met

2822 2852
TTT GGC ACC TAT TTT CGT GTT GGT TTT TAT GGA ACC AAG TTC GGG GAT TTG GAT GAA CAA
phe gly thr tyr phe arg val gly phe tyr gly thr lys phe gly asp leu asp glu gln

2882 2912
GAA TTT GTT TAC AAG GAG CCT GCA ATA ACC AAA CTT GCA GAG ATA TCT CAC AGA TTG GAG
glu phe val tyr lys glu pro ala ile thr lys leu ala glu ile ser his arg leu glu
↓ ref 10.1 and 10.2

2945 2972
GGA TTT TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT GAA GTA ATC AAA GAC TCT AAT CCT
gly phe tyr gly glu arg phe gly glu asp val val glu val ile lys asp ser asn pro

3002 3032
GTA GAC AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT ATT CAG ATT ACC TAT GTG GAG CCA
val asp lys cys lys leu asp pro asn lys ala tyr ile gln ile thr tyr val glu pro

3062 3092
TAC TTT GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC TAT TTC GAC AAA AAT TAC AAT CTT
tyr phe asp thr tyr glu met lys asp arg ile thr tyr phe asp lys asn tyr asn leu

3122 3152
CGT CGA TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT GGC CGT GCC CAT GGG GAA CTT CAT
arg arg phe met tyr cys thr pro phe thr leu asp gly arg ala his gly glu leu his

3182 3212
GAA CAA TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT CAT GCC TTT CCT TAT ATT AAA ACA
glu gln phe lys arg lys thr ile leu thr thr ser his ala phe pro tyr ile lys thr
↓ ref 11.1

3242 3272
AGG GTC AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA ACA CCA ATT GAA GTT GCT ATT GAG
arg val asn val thr his lys glu glu ile ile leu thr pro ile glu val ala ile glu

3302 3332
GAC ATG CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA ACA CAT CAG GAT CCC GCA GAC CCC
asp met gln lys lys thr gln glu leu ala phe ala thr his gln asp pro ala asp pro

3362 3392
AAA ATG CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC ACC ACA GTG AAT CAG GGG CCT TTG
lys met leu gln met val leu gln gly ser val gly thr thr val asn gln gly pro leu

3422 3452
GAA GTT GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT GAC CCA AAG CTC TTC AGA CAT CAT
glu val ala gln val phe leu ser glu ile pro ser asp pro lys leu phe arg his his

3482 3512
AAT AAA CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA AGG TGT GAA GAT GCC TTA AGA AAA
asn lys leu arg leu cys phe lys asp phe thr lys arg cys glu asp ala leu arg lys

3542 3572
AAT AAG AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT CAA AGG GAA TTG GGG AAA CTA TCT
asn lys ser leu ile gly pro val gln lys glu tyr gln arg glu leu gly lys leu ser

3602 3632
TCG CCT TAA AGA GGC CCT ACA GCC CTA GAT CAC AGA AAG TCC CTC AGT TAT CCA AGC CAG
ser pro OCH

3662 3692
TAT TGC TTG TCC CCT GCC ACA GAG ATT CCT TCA GTC GAA TGA GCT TTC GCA AAA TGG ATC

3722 3752
TCT AAA CTG AAT GCA CTT GTT TTA TTC ATC TGC AAA GAG CCA TGT ATT CAA CAT CGA GTG

3782 3812
TGA AAA GAT CTA TTG GAA ACC AAC ATG GAA TGG AAT TCT GGA AAT TAT TAT TCA TTG AAG

3842 3872
AAT GCA GTG GCC AAG AAA ATA TCA AAT GTA GAT TGT TAA CGC TTG AGA ATC ATG GCT ATG

3902 3932
GTT TCT AAT GTT CGG GTA ACA AGC TGT TAT CTT TTA AGA CAT TTT AAT GAC TCA AAG GTA

3962 3992
CAC TAT ACA TTT ACC ATT ATT TAT ACC ATA GCT AAG GTT AAA AAT TTA TTC ACT TTA AGT

4022 4052
TCG TAT TTT TTA ATT TAT ATC ACC ATT TAT AGA TTC ATT TTG GAC CCA TTT TAA ATG TAG
ref 12.1

4082 4112
TAA TGC TTA TTT TAA AGG TAC TAA AAA ATA TGT GAA TGT TTA CCT CGT GCG CGC CAG GGC

4142
CTC

Ref 1.1

Sequence of BAC8 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 364-380.

TTTTTTGAATTAATGGTGAGCAAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTG
AACAAATTTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAAC
GCTTTTCCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGT
GGACACTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTC
TCAGGGATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTG
CTAGTCATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGG
AAAGAGCTTTATAGATAACCCACTGCTATTGTTATGGCTAGTAAACCCTTAGGGAAATG
CCAGTTACAATCAATAAAAAAACAACAGTCTGGCTGGGTGCAGTGGCTCACACCTGTA
ATCTCAGCACTTTAGAAGGCCGAGGCAGGAGGATCACTTGAGATCAGGAGTTTGAGAC
CCAGCCTGGGCAACATAGCAAGAGCCCATATNTACCCAAAAAAAATTTTTTTTTTAAAT
TAAGCTAAAACCCTGGNNGGCCACAAAACCTGTAGTTCCCATCTACTTTGGAAAGGCT
TGAAGGANGGGAGGGCTTGCTTTGAGCCCCAAGAANGTTCAAAGGCTNGCNGNCAGG
TTNTGATTGNACACNTGCAACTCCCGCATTGGGTNAACAAAANCCAAGGAANC.

Ref 1.2

Sequence of BAC9 using primer C3S3, which spans nucleotides 340-359 of the cDNA. Exon sequence is underlined and represents nucleotides 371-380.

AATTAATGGTGAGCAAAAACTGAGCATGTTCTTTAATATTTTTTCTCTTAGTGAACAAT
TTTATGCTAGCTCATTTGTTACCTTAGAAATCTTTTTCTGTTGCACATCTTAACGCTTTT
CCATGTGCCTCTAAGACAAAATTACATGTGTTACATCTCTAAATAAACACTGTGGACA
CTCAACACAGTTTAGGTGGAATTAAGAGTGAGGCTCATTTTAACTCTTATTTTCTCAGG
GATGGTTGCATAAGCTAGCTATATTTTCAAAGGAACTTGTGATACATTCTTTGCTAGT
CATTATACATGAAGTGTATAATGACAGTATTGTAGATTTTATACCAAAGATGGAAAGA
GCTTTATAGATAACCCACTGCTATTGTTNTGGCTAGTAAACCCTTANGGAAATGCCAGTT
NCAATCAATAAAAAAACAACAGTACTGGCTGGGTGCAGTGGCTTACACCTGTAATCTC
AGCACTTTATAAGGCCCNAGGCNAGGAGGATCACTTNAGATCCAGGAGTTTGAGACCAG
CCTGGGCAACATANCAAGAGCCCATATCTACCAAAAAAANTTTTTTTTTTAAATTAAG
CTAAACNCTGGGTGGNACAAACCTGTTNGNTTCCNATNTNCCTTTGGAAAAGCTTANG
AAGGGGAGGGCTTNCTTTGGANCCCCAAAAAGTTNAAAGGGNTTGCAGTCAGCCTTTT
NAATCACCCNNGGNCCTNTCGCATTGGGATTNCCAANANGCCAANGNAACCCCGNT
CNTNTTTTAAAAAANTNTTTTAAAGNANNTTTNTTNGN

Ref 2.1

Sequence of BAC8 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is underlined and represents nucleotides 381-385.

TCTTTNNGAAAAAGATTANATTATTAATTCTATGATATATTAACAATACACANCTCTAA
CACTTGGACTATTTTTAAAATATGGCATGTAATTTAATAGATGACTGAAATATTTTAGC
TTCTCAAATATTTTTTAAAGTTCCTACAATGTTTTGTATTTGCTTAAAATAAAATANA
AAAACCATATTAATCTTTCAGAAAATTATGCTAGCTAACAATAGGACAAAAAATTCT
GTGTATGTCAACAAAAAATTCAACCTTAAATTTTTTTTTTCCATAAAAAACAGGGC
TACTTGCCCAGGTGAGANGTGCTGCCGTATGAGCTCCTCGNTAGATTGCGCNGCCGGA
NTGTCGGNCCCTNCGTTTAATATAACGGCGTGNGCNTGTACCGCAGGCTNTGCTAGGT
CGTGNTCCCAAGATATCNTNTNTANCATANTAGACGNTGGNGNCGNNTGCATGTGGCN
TNATTNTNGCAATTGTNACAATCCTAGTNTGTACNTNANAGNTCNGCCNCTGTGANNT
CGTTGTATAGTCNGNGGCNCGCTTGNTTCTGATGCTGAGAGCANTNNCINNACTNTTNN
NCNCCCATCTTTNCNNTTNNNNNCCCCCNNTTNNATNNTTTNNNTNNCINNNTNNATNT
NTNAANNACCNC

Ref 2.2

Sequence of BAC9 using primer HC3AS7, which spans nucleotides 386-405 of the cDNA. Exon sequence is not found within this sequence. Since the primer is directed against exon sequence we presume that sequence derived from HC3AS7 is intron sequence. Additionally, this sequence matches the intron sequence found in the previous sequence (BAC8 sequenced with HC3AS7).

GCGCTNCCNNNTNNTTTATCTTCTGAAAAGACTNATATNATTCTATGATTATAACATTA
CACACTCTAACACTGGACTTNTTAAATATGGATGTAATTAATAGATGACTGAATATTTT
AGCTTCTCAAATATNTTTAANGTCCCTACAATGTTTGNATNTGCTTAAAATAAAATANA
AAACCCCATATTAATCTTTCAGAAAANTATGCTAGCTAACAATAGGACANAAAAATTCTG
TGTATGCAACAAAAAATTCAACCTTNAATCTTCTTTTTTTTCCAATANAAAAACAGG
GCTACTCTGCCACAGGCTGGAGTCAGTGGCTGATACAGCTACTGCAGCTCACTCCGGG
CTATGTGATTGCCTGCCTAAGCCTCNGAGTAGTAGGCTCAGGTGCCACTACATGCCAG
TAATCTAAAATTTATAGAGACAGGGCTGCTGTGTGNCCAGGCTGGCTAACTCCGGGCT
AAGCGTTCTTGCTNGCTCTAAATGTGGGATACAGNATGTATCATNCATCAGCCAAAA
AGTTAATTAANTTCCAGATNANTATTTGCATCAAAGCTCCAATNTAGCTTGAAGTAGA
ACCTGCTCNTTGGCTAGANTATCCCGNNTGTTATGGATCATATTANGCNNTTGTGATGC
CGAATGGNATCTATTCCGGGAGACANATTAATCTATNGGATGANAGCANATNGCCCNAT
GCTTNTTTGTAACGCTNNANNTAAGAACNTTCTNGACATCGTCATAGNTCGAAGTNT
NNGCGANTTGATACTAANTTCATGNTANGCCNATGACTNTNGTGATTNNTGANTGNCT
GGGAGAACCTACNTNCCCCNTACNNATANNCTNCACCCCCTACTACTNTNNCINNNTCNC
TCTCTANTTCTACTCCACNTTATTATCCTCINNCTTCNCATCNTCCCATCNTNATTCNAC
GCCNCNANACTTANCNTTATNCACTCTNNCT

Ref 3.1

Sequence of BAC8 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-733.

TAATGTACATAGTGCTCATGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACA
CCAGAACACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCA
TAAGTAAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCA
AATTAGAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCA
GTATCACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACT
GTATAAACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAA
TATTTCTACTTCTCATAAAACAGGGAAAACGTATATCACCAAAAATAACTTCTTATTAC
TTCCTTCTTAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCTGTATTTAT
AATTTGTCTGTTTTCTCAGCAACATCATAAGCTACTTGAGGAGACATACTATAAACTGA
TTTAACAGCTTTAGTGTCCCTACAGCTTAGCTCAATGTTTGACAAATATAGGAGATCAA
TGCTTAAAGGAATAAAGGCCAGGACAAGTTCTGGTAGCAAATAGTCCATAAAAGGTTT
TGGGGGAAAAGGGTAAAAATGGATACATATCGGGGTNGCAAGNTTTTTCCATGTGGG
GTGAGGTGCCCCATGCCTT

Ref 3.2

Sequence of BAC9 using primer C3AS4, which spans nucleotides 737-756 of the cDNA. Exon sequence is underlined and represents nucleotides 677-730.

TAACATAGTGCTCTGACTGCAGATGATTCGTAGAAAATCCAGCCTCAAGGACACCAGA
AACTGGGATTCGGTAATGAGTAAAGCTTTGAAGACACCTTGTAAGCAATGCATAAGT
AAGAGAACACCAATTGAATCTATTATTTCTTTAATACTAATACCAGAATGGCAAATTA
GAATTAAAGAGATAGTACTTGGTATCCAGTTTGGGTTTTGTGGCTTAAGTAGCAGTATC
ACCTTTTTCCAGAGTTACTGCTAAAATTAAAAATTTTAACTATCAGGTTTACTGTATA
AACATATTTGACTAACCTAAAAGCCACATTCTTGTATTTCCAATATAGCATCAATATTT
CTACTTCTCATAAAACAGGGAAAACGTATNTCACCAAAAATAACTTCTTATTACTTCCT
TCTTAAAAAGAAATTATCAATTCTTTTTATAGCACTTTGTGCTTACCCTGNATTTATAAT
TTGNCTGNTTTTCTCAGCAAACATCATAAGCTACTTGAGGGAGACATACTATTAAACCT
GATTACAGCTTTTANGTGTCCCTACAGCTTAACTCAATGTTTTGCAAAATNTNNGGAGA
TCAATGGCTTTAAAGAATAAAAGANCAGGGACAAGTTNTGGGTNGCCATNAGNACAA
TAAAGGTTTTNNGGGGAAAAGGGGAAAAAATNGATTNCATNTCGNNGGTNGCAAGGTN
TTTTCCATTGNGGGGNGGAGGGGCCCATGCCATAANTTTTAACCTTTCTTTTTTNGAAG
AAATTAAACNNTTAAAGGGGTN

Ref 4.1

Sequence of BAC8 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-917.

CCAGTCTGCAATATGCTGTGCGAAGCCGATATCAACTTTGCATCTTTGTCTTGNCATTC
GAGAAATCAGACTTGTGGAAGTAGGAGACAGCTTACAGCGTGCACAAGCTCTCAGCA
 GAGCATATACGAATGAATCTTTTCCAGGGAGTTATTTATATACTACCTGAGCAAGCCA
 CTTTAGCTTTGGGCAGGAACCTTNTGGATGTTATAAGTAATACTTATATGAATAATATGA
 AATTAATATTTACTTCTTTTACANTCTTCTCTTTTCCTTATCTTAGCCTTTATCCCCTTGT
 GGAAAAGACACTATCAATGCTAGATNCTCCCAAGNCAGAGAATTATGCAGGTTTGGTC
 AGAGAATCGACACAGACATGTTTACAGATTCTTCTTGAAATACATATTGTGCACGAGT
 TTTTACANTATCTCAATTTAGATCTCAGACAGCATNTNGACTAGNGGGTCTAGGACAT
 AGATACATNTTTGNGAACTTCTATAGAANAACNTNTGCNTTAAAAAGGAGCTTGTTNG
 ANANGAATNNNCTGNGAAGGGCCCGATACGANAATTTGACTTCGGNGAAAATTNNNG
 GATTNNTACAAANTTCTAGGNGGCACCTTNAAAANGNNTGGGNACNTTGGNGGCGGA
 AAAAAAGCCCTTCNTTtagTNTCCCNGAAATGGAAAAGTNCCAANTTCCNAAAAAA
 ANGGGCTTTGTTNNCTTNCNANA

Ref 4.2

Sequence of BAC9 using primer HC3AS6, which spans nucleotides 924-944 of the cDNA. Exon sequence is underlined and represents nucleotides 802-921.

GACGCCAGCTCTGTACACAGTCTGCAATATGCTGTGCGGAAGGCCGATATCAACTATT
GCATCTTTGTCTNGNCATCGAGAAATCAGACTCTGTGGAAGNAGGCAGACAAGACTAT
ACAGCNTGCACANAGCATCTCAGCAGGCATATAAGAATGAANCTTTTCCAGGGAGTTA
 TTTATATACTACCTGAGCAAGNACTTCAACTTNGGCAGGAACCTTGTGGATGNTTATAA
 GTATACTTATATGAATAANATNGAAATTAATATTTAATTCTTTTACTTCTTCTTTTCC
 TTATCTTAGCCTTTATCCCCTCGTGAAAAAGAGCACTAATCAATGCTATTNCTNCCAAG
 NCAGGAATTTATAGCAGGTTGGTCGAGAATCGACACGACATGTTTACAGANTCATCTT
 GAATACATNATTGTGCACGAGTNTTTTACTCTATCTCAAAATATAGATCTCAGATCGTC
 TATNGANTATGNGGTTCTAGGACATGATTACATTTTNGGGAACCTTCCATAGAATAAA
 CNTNTACCTNAAAAANANGAGCCTGTTNGAAATNGAATCTACTNCTAAAGGGCNAGTNC
 CANATTTTACTTCCGCGANATNTCNGGATGTTACAAGTCTAGGGGGNCTTTAGNACGT
 TNGATNTTTGANCGGAAAAAAGCCCTTCTANNGGTCNCCTAATGGAAGCGCCAATTCC
 NAANAAGGNCTGTGTTNTTNGACATTTACCNNGNCCNTTTCTAATCAAACNTNCTCTTC
 TNNANCCNCANCN CNNNCCTATANNCCCTATCNCTCNCTNNTNNTCNTCACTCTCNC
 NCTNTCTTCNTTCTNCACTNTNNNNTCNCTNNNATNNNCTTCTCCNATCCNTCTCANN
 NNNTCANNCTCCCTACNNTNCNCNTNTTACCATCTNCNCCNNCCT

Ref 5.1

Sequence of BAC8 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1181-1269.

GTATGATCCGCCAGACCGCTGCCATGGCAATNGTAGGGACATCGGTCCCTCAACTAAC
AAGGCCTGGCAGTTTCTNCTCACGTCAACGGTCAAAACAATCCTTCTACAGAATTTT

TTTTCTNGAAAGACAAATATTTACTAGGATATGCCCTTAAATATATGAGATGATTGTAT
 CAGCTGATGCAAAAAGTGCTCAGTTTTATTTATGAAAATATTAAGTTCCCAGAATATTA
 ACTGTCTTCTCCCAAACAGTTTTTAAAAAATGATTACCTCAAGGTTTATGGGAAAAAGC
 CCCGTAATTCTGCATTCAGAATTTGGAAAAATTGCCTCATTATAGATAGCCATNTCTTTTTT
 TTNTTTTTTTTTATNCTTCAAGTCTTAGGGNACATGTGCACAACATGCAGGNTAGTTACA
 TATGTATACATGTGCCATGTTGGTGTGCTGCACCCANNAACCCGCAATTTAACATTAGG
 TNTATCTCCAAATGCTATCCNTTCACCCTTCCCCCATNCCACAACAAGGCCCCGGGCNT
 TGNGATGTTCCCCTTCCTGTGCCCACTGTGTNTCACATTNCCNCTTCCCNCCCTTANTN
 NNGTGCAGAACNTNGCCNGTNGCCCTNTNTTTTTTNCCCC

Ref 5.2

Sequence of BAC9 using primer C3S6, which spans nucleotides 1127-1146 of the cDNA. Exon sequence is underlined and represents nucleotides 1151-1269.

CCNCTGATGATTATGAAAGTGAGAGCGGAAGTATGATAAGCCAGACCGTTGCCATGGC
AATCGCAGGGACATCGGTCCCTCAACTAACAAGGCCTGGCAGTTTCCTCCTCACGTCA
ACGGTAAAAACAATCCTCCTACAGAATTTTTTTTCTAGAAAGACAAATATTTACTAGG
 ATATGCCCTTAAATATATGAGATGATTGTATCAGCTTGATGCAAAAAGTGCTCAGGTTT
 ATTTATGAAAATATTAAGTTCCAGAATATTTAACTGTCTTCTCCCAACAGTTTAAAA
 AATGATACCTCAGGTTTATGGGGAAAAAAGCCCCGTATTCTGTCAATTCAGAAATTTGG
 AAAATTTGNCTCATTATAGATAGTTCATTTTCTTTTTTTTTTTTTTTTTTATACNTTAA
 AGTTTTTAAGGGGNACCATGTTGCACCAAANATTGCAGGGGTTNGGTTACCATTATGG
 TTATTNCCATTGGTNCCCCCANTGTTTGGGGNGTTGGCTTTGCCACCCCCCAGNGTAAA
 ACCNNCCGNTGCGAATTTTAAACAANTTTGGGGGTTATTANTTNTTCCCAAAAAT
 NGGCNTTTTTNCCCTTTNCCCCCCTTTNCCCNCCCNNTTCCCAACNNANCAAGGGGCC
 CCCCGGGTANTGGGGGAATAGNTTCCCCCCTTNCCCTNGNNGGGCCAATTGTGGGG
 NNNCTCCATTTGGNNTGCAAANTTCCCCCACCNTNATTGTTGGTGGNGAAACCATTTC
 CCGGGGGGTTTGGGGGTTTTTTTTTGGTCCCNTTGCCCAANTAATTTTGCNTTGAANA
 AAAAGAATGGGGTTTTCCAAAGCTTTTNGTCNCCATTTGNTCCCTTTANGGNCCNTTN
 GTTCNCCTTNCCANAANGGGCCAATGTGAAACNNCCTTTCATTTTTTTTTTATTGGGGNT
 TNCCNTTATGGN

Ref 6.1

Sequence of BAC8 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1535-1588.

TTCTTGGGAGCATAGGTGCCAGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCG
 GTACGTACACAATAGCTTCTCCTCCTGGTGAGAATTTCTTCAATTTCCCTTGAGTTGTAT
 ATTGTAATGATCATTGTTGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTT
 TAAGTGTAAGTGTGAATTAAGTGAATAATCATTCTCTGCAGTAATAAAAGTTAGAAT

TCTGATTTAGGTGAGTCAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTC
TAGAAAACGTTCTCTAGAAAGTCCTATCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTG
ATTAATAGCATCCATCCTCCCTTTTTAAATAGACTTTATTTTTGTAGAGCAGTTTTAAGT
TCACAGCAAAAGTGAGCAAAGGTACAGAGATTTCCCATATACCCCTTAGTATGCGTAG
CCTCCCCCATTATTAACATCCCCCATCAAGAGTAGTGCATTTGTTGTAAGTGGTGAACC
TACATTAACACATCATCACCCAGAGTCCGCAGTTTACATTAGGGATCATTATATAACA
TCTATTTTTACTTTTTTTTTTTTAGTTGAGACAAGATTCTCGCTCTGTACCCAAGCTGG
AGTGCAGTCCGNGTGGATTGTNGGCTTACTGNCN

Ref 6.2

Sequence of BAC9 using primer C3S7, which spans nucleotides 1513-1532 of the cDNA. Exon sequence is underlined and represents nucleotides 1547-1588.

GTGCCGGCAAGAAATGGTACGGCGAAGCCGAGGACAGCTCGGTACGTACACAATAGC
TTCTCCTCCTGGTGAGAATTTCTTCAATTTCTTGAGTTGTATATTGTAATGATCATTGT
TGCTAGTCTTCAATGTCAATCCTATGCTTTTTAAAAAGTGTTTTAAGTGTAAGTGNAA
TTAACTTGAATAATCATTTCTCTGCAGTAATAAAAGTTAGAATTCTGATTTAGGTGAGT
CAGCATACCGCCCCCCCCCGTTTTCTCTAGAAAGTCTTCTCTAGAAAACGTTCTCTA
GAAAGTCCTCTCTAGAAAACCTTTCTCTAGAAAGTCCTTATGTGATTAATAGCATCCATC
CTCCCTTTTTAAATAAGACTTTATTTTTGTAGAGCAGTTTTAAGTTCACAGCAAAAGTG
AGCAAAGGGCAGAGATTTCCCATATACCCCTTAGTATGCGTAGCCTCCCCCATTATTA
CATCCCCATCAGAGTAAGNGCATTTGTTGTAAGTGGNGAACCTACAATTNACACATTN
TNACCCACAGTCCCGCAGGTTTACATTTATGGGATCATTCCCCTANTAACACCTATTT
TTTTACTTTTTTTTTTTTTTAGGTTGAGACAAGAATTTTCGGCTTCTTGTGTACCCCCAA
ACTNGGTAGTAGNCNNACCGTCGNGNAATTTNTGGGGTTTCNTNGNGNNCANTTTGTG
CNNTCNNCTTNNCNCNAAAGAANTTTTTTTTACCCTTTTTTTCCCCCNAANANANN
ANCCTTCCCCTTGGNGGANGCTGGGGACTTCCNCAGNGGNGG

Ref 7.1

Sequence of BAC8 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1861-1917.

CAAAGTGCAGTTTATCTCAAACTGTTTTGCTCACAGAGAGCCTTGGTTTTCAAAGGTAG
GTTATTTTGTACCTGCAGTGTTGTCAGACTTTGTTTTTTTTATTAACATTGTCTAAGATC
ATTTGACACATTCAATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAA
AATTTAAATAATAACCTAAGACCCTTAATTCCTTCTTGCCTCTCTACTGCTGCCTGCCTT
TTAGAATTTTTCATTTATTCGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAAC
TTGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTG
TTTTCTCTTCACTTGGTTCTGTTTTTATAAAAACTCAATTTATAAAGAATTCAATATAT
AAGCAATTCAACCCACTGAAATTATTTTATGATGAATGGAAAAGAAGGTATGTGTTTG
TTCAACTGCTTTAAATGTTTACTTCTTATATTTGTTTTCCCTTAGAAATATGTATATTCTT

AAATTTTGAAGGTAGCTATTTCAATTTAATCATCCTAGAGGATGGAATGCANAGATGTT
GGATGAAAATAACTTACGTATTATTTTGTAAATAAATAAGAATTCATATATGGTTGAT
TACCTAAGTGGTTTTATGCACATTCTGATAGAAAGCTTCACCAACAATCCCTTGNTNGA
TATATTATTT

Ref 7.2

Sequence of BAC9 using primer C3S8, which spans nucleotides 1842-1860 of the cDNA. Exon sequence is underlined and represents nucleotides 1864-1917.

AAGTCAGTTTATCTACAACACTGTTTTGCTACACAGAGAGCCTTGGTTTTCAAAGGTAGG
TTATTTTGTACCTGCAGTGTGTCAGACTTTGTTTTTTTTTATTAACATTGTCTAAGATCA
TTTGACACATTCATTGGTTAATATATGTAGTAATATATTAATGAATATGTGTAGTTAAA
ATTTAAATAATAACCTAAGACCCCTTAATTCTTCTTGCCTCTCTACTGCTGCCTGCCTTT
TAGAATTTTTTCATTTATTCTGAATCACCTTTAACCAGTTCTGGTTTGAAAAACAGTAACT
TGGATGTGGAGAAGGGCCTGAAATTAATAGCCAATCTTAAATATGGGGCTTCTCTTGN
TTTCTCTTCACTTGGTTCTGTTTTTATAAAAAAATCAATTTATAAGAATTCAATATATA
AGCCATTACCCACTGAAATTATTTTATGATGAATGGAAAAGAAAGGTATGTGTTTGT
CACCTGCTTTAAAATGNGACNTCNTAATATTTTGGNTTCCCTTAAGAAAATATGTAT
AATCCTTAAAANTTTNGAAAGGGANGCTANTTTCAATTTTTTNAATCAATCCTAANAGG
GATTGGGAAATGCNCAAGATTTTTTGATTGAAAAANAACCTTANCGNATTTAATTTTTN
GGNAATAAAATAATTAGNAATTCCNTATTATGNTTNGAATTACCTAAAGTGGTTTTTAT
TGCCCCATTTTNTTGATATGNAAAGCCTTTACCAACCAAATTCCCCNTTGNNAAGGAAT
ATTATTTTTTTNANGGGCCTCNTNTTGTGGGGNTGGAAGNAAAAACCTTTGTTCCAAAG
GGTCCCCNC

Ref 8.1

Sequence of BAC8 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2432-2523.

AGTGCTAGTCCTCAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAA
ATATCTTCCTGTGGGATGTGTAACATTTCAAGGTAGGAATCTTCCAGATGTACATTAAAT
CAAGGTATATCTTTTTTTGGTTTTAGCTTTTCTCACTGGTGTTTAGATTTTTTTAGTTTAT
AAGGAAAGCTTAAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTACAGTG
ATTGTCATTAATACATTTTTAAGGAGTACTTCTTGTTGATTCTCTTCCACAGTTTCTTA
CCTCTGAATTATCAGCACTATGCTTATTTATTCTCTTTGGCTTTACTGNCTTGNAATCCC
GTTACATACTTTAACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATT
CTTAATTGGCTTTTACTTCACATAGCAGATATACCAACATTCTCTATTCCCTACATAAA
ATATTAAGATTATTTTATGACTAATACCCATGACTCACAGATGAGTTTGCCCTCTAGTA
GGGTCATAATTCTGACCCACTAGTTGAATTCTCTGCTTACCAAGAGNCAGGTATGCTTG
CTTTTTCTTCAAAACCTGTAAATAGTAGGNTTGGGGATATTNTAAAAATTAGGTAAAT
GGTATATCTTCTGGTGGAAANCAGAAAN

Ref 8.2

Sequence of BAC9 using primer C3S10, which spans nucleotides 2412-2431 of the cDNA. Exon sequence is underlined and represents nucleotides 2444-2523.

CAGCAGCACTTGTTGCTGAATATTTGAGCATGCTGGAGGACCGGAAATATCTTCCTGT
GGGATGTGTAACATTTAGGTAGGAATCTTCCAGATGTACATTAAATCAAGGTATATC
TTTTTTGGTTTTAGCTTTTCTCACTGGTGTGTTAGATTTTTTTAGTTTATAAGGAAAGCTT
AAAGACTTAAGCCAATGCTTCACAAGGTGAATTAACATTTACAGTGATTGTCATTAA
TACATTTTTAAGGAGTACTTCTTGTTGATTCTCTTCCACAGTTTCTTACCTCTGAATTA
TCAGCACTATGCTTATTTATTCTCTTTGTCTTTACTGCCTTGTAATCCGTTACATACTTT
AACATCTATGGAAATGTATTACTGATAATCAGAATTCAGTAGAAATTCTTAATTGGCTT
NTTACTTCACATAGCAGATNTACCAACATTCTCTATTCCCTACATAAAATATTAGGATT
ATTTTATGACTAATACCATGACTCACAGATTGAGTTTGCCCTCTANTAGGGTNCATAAT
TTCTGACCCACTAGTTGAATTCTCTGCTTACCAAAAAGTCANTTATGCCTTTGCTTTTTCT
TCAAAACCTGNTTAATTAGGNACGGCTTTGGAGATAATTTATAAAAAAATTTCAAGCT.
NAAANTGGNTTATTATTCNTTCCNNGGTTGAAAAAACCCAGGAATTGGCACAAANNAA
NAAAAAGNTTATTCCNNGGTTTCTTNCGGNAAAAAACCAAAAAATCTTNGAAATTGT
TTTTTACCAAAAANGACCTCCNCNGGGAAAAAGGGNGTAAATTTNTTCCNTAAAAACN

N

Ref 9.1

Sequence of BAC9 using primer C3S11, which spans nucleotides 2679-2698 of the cDNA. Exon sequence is underlined and represents nucleotides 2711-2799.

TTCCTATTCATGAAGCTAATCGGGATGCAAAGAACTATCCACAATTCATGGTAAACT
TCAAGAAGCATTAGCAAAAATTGTTTCATCAGGTAATGATTCCAATTTCTAGCTTCACTA
TAAAGGGAAAAAACTGTCTGAAAGCATTAATGTTGTTTTGCACTGATGTCAAACCTAGA
TCCCGTGAAATGACCATTTTAATCAGACTACAAATGAGCGGTCAAAATGATAGTTCAT
GGCCAAAGCAAAGCTCATTAACAATAAAAAATGAATTCACCTAAAGTAAATGGTGATCA
TCATAAACTTTCTGCATAGCTTTTTTTTTTTTTCATTTTTGAATTATTAATTAAGCAAGTTTT
TAAAAATTGTGATTTTTCTGTTTCACAAGGNAAGATCATAAGTTGNGGAATCTCATTTTT
AAAAATTGATACCTATTNCTTTTCTGCTGNGGAAAANTGGAAGTTTTTTAATATTTTCAA
GGTTTTTTTTTAAATTNAAATGGATTGTGGAAAACCTTTTAAATNAATTTAAACCTAC
CTAAAATANTTTTTTTAATGGNCCNNGCCANCTGGAACCNTTTTATTTTTTTCCCTAG
GAATGGTTTTACCAAATCCATTCCCTTTTGAATAATATTTTTCCCTNAATTNCCCCAA
AAANTTTTTNTTTTTTTGGGNGGAAAAAATANTTGGAAAATTAATAAAAAATGGGGGTGG
GGCCNTAAATGGGGATTATTTTTAAATTTCTAAAAAAGGGANTTTTCCATTTACCTTT
NAATCCTTTTTGGGNGGNTTCNATTTATTGGGGAATCCTNCNCTTTTTNTNCNCCTTA
AAAAANTTAGGGCTNCCAAAATTTTAAACCNTTTAATTTTTNAAAANGGAAAGGGNC
CCCTTTCTTNGCCCGGTTGGTTT

Ref 10.1

Sequence of BAC8 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2928-2941.

TACAGATTGGAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCT
CTCTGATGATTAGACTTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAA
ATAAACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAAT
CTTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGAGACTATTTTCACACAT
ATTTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTA
TAATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTGAACTA
GAACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTT
CCAGGTGAGGTTTCTTTAGAACGTAAAAGCCTGAAATCACACCTTAAAAACACTTCCT
TTAACCTTTATAATTTCTTAATTTTCACCATAAATGATTGCGTTTTATATTTACTGGGGC
TAACTAGNATTTTCTGNTATAGGTATTCTTTCCAACCTTTCTCTATTTTTTGTACTCAA
AGTGTAGTGGATGGACCGGAAGCATTGGGGTTACCTGGGAGAATGGTTGGNAATGC
AGAACCCTTAGACCCCAACCCAGCCCCTGTGAAA

Ref 10.2

Sequence of BAC9 using primer C3S12, which spans nucleotides 2908-2927 of the cDNA. Exon sequence is underlined and represents nucleotides 2930-2941.

CAGATAGTAGGTGAATGCTGTGGTGGTTCATAAAATGTCATCTTTAGTTTGTATTCTCT
CTGATGATTAGACTTTTCAGATCCAGATCTAATCATTTAGTAAGCCAGATCTTGCCAAAT
AACTACTCCGTTAGAGAATAAGGACTTTTAATAGTTACAATAATACTCTTTCAAATCT
TTTATGGCAGCAATAAAATAGTAATATTGTCTATTTTTTGAGACTATTTTCACACATAT
TTTAGAAACCCCTGTATCCTTCAGAATTACTGCGACTTAACGGAGAAATATATAGTATA
ATCCCACATTTTGTGAAAAAGACAAAGAATTAAGTAGTAGCTAATAATTTGAACTAG
AACCAGAACCCTAAGAAATTTCTGACCCAAGCATATTATCTCTTTGGCTTAACTGGTTC
CAGGNGAGGTATCTTTAGAACGTNAAAGCCTGAAATCACACCTTAAAAACACTTNCTT
TAACCTTTATAANTTNCTTAATTTTCACCCATAAATNGATTGCNGTTTTATATTTTAC
CTNNGGNCTANACCTNAGGCAATTTTCTGGGTCATAAGGGAAATTTCTTTTCCCAA
CCCTTTTCTTATTTTGTGTTGGGNCACTCCCAAAGGTGNTCNGTTGGGGNTTNGGG
NCCCCGNGAAAGGCCATTTGGGGGNTTACCCCCGGGGGANGATTTGGTTTTGAAAA
TNGTCNNNAAAACCTTCCNNAACCCCNCCCCCNGGCCCCCNNGNNNGGAAATCCAAA
AGGATCTTGNCNATTTTTTTANCCAAANGANCNCCCCCNAGGGNNGGGATTTTNGTTAT
TTCCCAANAAGANGTAAGGTTNTTGGCCTTTNNGGGCNTTGGGTGTTTTNTTTNN

Ref 11.1

Bac 9 sequenced with HC3AS3, which spans nucleotides 3376-3393 of the cDNA. Exon sequence is underlined and represents nucleotides 3267-3289.

CTGANGTGTNGCAANGCCACTCCTGTGTCTTTTCTGCATGTCCTCAATAGCAACTTCAA
TCGGTGTTAAGATGATCTGAGTNANNGAGCATCTGTTANATCAGNGTACTGACTGAAA
 CTATTTAATGAACTTTATGTATAATCAACTGAAATTAGANAAAAAAGATCAATNGT
 AAAC TTCATGTAAACAATAAAATTCCAAACTTGGATTCTAAATGAANNAAAAANATCAA
 CCTTTAAAGAAAAGCTGGGGGTGAATAAGGGCTTAGAAAAGANGTANAAAATGANGA
 CTCAAAATGGTAAAGGGTCTAATATGNATGGATAAGGATGGACATATCTTCGGACTCT
 GAGTGGTGTACATGGCTTGATGATTGCTCACTATGTGTGNCATTATGGCTACCTCTCTT
 TAGGCATGCCTGTTAANTAGGAAGCTGAACTANCAAAGNCTCTTNGATGTATNANTCC
 TGCCGCTNAAGAAGGGGNCGCNTGANNCAAATGATTTGCNATGTNTCTGCTATNATNG
 NAAGNGNTCCTNGANTNNTTCNGANAAANCTCTCNANGAGNCTAGTTTACATNCGGTC
 AGNGCTTCTTGACCTCCTGNGCATCTCCCGTANTTCACCCTCATTNNACCNTNANTTT
 ATAANNANNNAGCCACNTNNCCTATAGGCNATCNACGCNNTTCCCNNTANTCANTNN
 NAGACAATTTTTTNNCGCCCCCTCTNNTCCTTCTNCTTCCNCCCNNCNCNCCCTNTN
 TCTNTNCCCCCNCCNNTTCTTANCTTNT

Ref 12.1

Sequence of BAC9 using primer C3S15, which spans nucleotides 3750-3769 of the cDNA. Exon
 sequence is underlined and represents nucleotides 3779-4118, and also represent the 3' terminus of
 the transcriptional unit.

TGTGAAAAGATCTATTGGAAAACAACATGGAATGGAATTCTGGAAATTATTATTNATT
GAAGAATGCAGTGGCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATG
GCTATGGTTTTCTAATGTTCTGGTAACAAGCTGTTATCTTTAAGACATTTTAATGACTC
AAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTAAAAATTTATTCA
CTTTAAGTTCGTATTTTTTAATTTATATTACCATTATAGATTCATTTTGGAACCATTTT
AAATGTAGTAATGCTTATTTTAAAGGTACTATTAAATATGTGAATGTTTACACTAATTT
 TACCGAGTGGGACTTCAAAATTTTTATTATTGACAATGGCTGAGAACAATTNAAGGGT
 TTGACTCNAGAACTANTTCCAAACCTAGCAGAATAAAAAATCATAGATAGCCCCAAATT
 AATGAGTTTGGGNAACTGTNTCAAAGTTTTTTTCCATTTACATACCCAAAAACAGGAA
 ATTTTAGAATTTGCCNGAACCTTTACCTTAAGANAAAAACCCTTTTGTGNTNAAAAATN
 TANTNTTAAAATTCCCGGGGGGANTAATCTTAATNACCCCGGGTGGGGCCANNCNCCC
 CNTTATAACTTTTGAATTTAAAAATTCNTTTTTNTNCAACCCCAAACCTGNANTNNGGGT
 NNTTTTNAAGGAAAACCTTTCCACTNGGAAGTTNNCTTTTAGGGNCCNANCCTNCNAN
 AAANNNGGGGAANATTGGGAAGTCTTCCCCTTCNTTNGGGGGGNGNCCCAAAAAATTCT
 TAATAAAANCCCCGGGGCTCCCATNTTAGNATTTTTTTTTTTGGCCCCACACTGTGTT
 NATTAANCCCCNCNTGCTAAAAATTTTTNNNGAAAANACCTNAACCCTTCTNNA

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPEKMAKLPVILGNLDTIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	-----VLHHHQNPFEFYDEIK
KIAA	KSAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTRSAFAAVLHHHQNPFEFYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHLLLLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----

HC2A	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA	PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSIISLISNSARV
HC5	-----

HC2A	OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVIILMQLFWLPNMIHEDDVPISCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5	-----

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HC2A      I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
KIAA      I I H V V A Q C H E E G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T K S M T T I L K P S A D F L T S N
rat      -----
HC4      L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
HC1      L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
HC3      T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G -- S V F --- E
HC5      -----

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HC2A	KLLRYSWFFFDVLIKSMAQHLIENSKVKLIRNQRF	PASYHHAAETVVNMLMPHITQKFGD
KIAA	KLLKYSWFFFDVLIKSMAQHLIENSKVKLIRNQRF	PASYHHAVEVVNMLMPHITQKFRD
rat	-----	-----
HC4	KLLKYSWFFFEIIAKSMATYLLEENKIKLTHGQRF	PKAYHHALHSLFLAIT-IVESQYAE
HC1	HVLKHSWFFFAIILKSMAQHLIDTNKIQLERPOR	FPESYQNELDNLVMVLSDHVIWKYKD
HC3	SALQQAFFFEFLVKSMVHHLYFNDKLEAPRKS	RFPERFMDDIAALVSTIASDIVSRFQK
HC5		

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HC2A      NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL
KIAA      NPEASKNANHSLAVFIKRCFTFMDRGFVFKQIN--NYIS--CFAPGDPKTLFEYKFEFL
rat       -----
HC4       IPKESRNVNYSLASFLKCCLTIMDRGFVFNLIN--DYIS--GFSPKDPKVLAEYKFEFL
HC1       ALEETRRATHSVARFLKRCFTFMDRGCVFKMVN--NYIS--MFSSGDLKTLCOYKFDL
HC3       DTEMVERLNTSLAFFLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVIVSLRLDFL
HC5

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HC2A      RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
KIAA      RVVCNHEHYIPLNLPM-----PFGKGRIQR-----YQDLQL---DYSLTDEF
rat       -----
HC4       QTICNHEHYIPLNLPM-----ATAKPKLQR-----VQDSNL---EYSLSEY
HC1       QEVCQHEHFIPLCLPIRSANIPDPLTPSES-----TQELHASDMPEYSVTNEF
HC3       RIICSHEHYVTNLNLPLTPASPSPSVSSATSQSSGFGSTNVQDKIANMFELS--VPF
HC5       -----MNADTAPSPCPSIS---SONSSSCSSFQDOKIASMFDRTSRVPA

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HC2A      CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
KIAA      CRNHFLVGILLREVG TALQEFRE----VRLIAISVLKNLLIKHSFDDRYASRSHQARIAT
rat       -----
HC4       CKHHFLVGILLRETSIALQDNYE----IRYTAISVIKNNLLIKHAFDTRYQHKNQQAIAQ
HC1       CRKHFLIGILLREVG FALQEDQD----VRHLALAVLKNLMAKHSFDDRYREPRKQAQIAS
HC3       RQSHYLGLVLTETLAVILDPDAEGLFGLHKVINMVHNLSSHSDSPRYSDPQIKARVAM
HC5       SSTSPGILFTETLAAALDAEGEGISEVORKAVSAIHSLLSSHDLPDPRCVKPEVKVKIAA

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HC2A      LYLPFLGGLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH
KIAA      LYLPFLGGLLIENVQRINVRDVSPFPVNAG-MTVKDESALPAVNPLVTPQKGSTLDNSLH
rat      -----
HC4      LYLPFVGLLLENIQRLAGRDTLYSCAAMPNSASRDEFPCG-----FTSP--AN--RGSL
HC1      LYMPLYGMLLDNMPRIYKLDLYPFTVNTSNQGSRDDSLSTNGGFQSQTAIKHANSVDTSFS
HC3      LYLPPLIGIMETVPQLYDFTETHNQRGRPICLATDDYESE-----SG---SMIS
HC5      LYLPVLGIIIDALPOLCYDFTVADTRRYR-----TSGSDEEQE-----GA---GAT

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HC2A KDLGAISSG~~AS~~PYTTTTPNINSVRNADSRGSLISTDSGNSLPERNSEKSN~~SLD~~HQSS
 KIAA KDLGAISSG~~IAS~~PYTTTTPNINSVRNADSRGSLISTDSGNSLPERNSEKSN~~SLD~~KHQSS
 rat -----
 HC4 TDKDTAYGSFQNG-----HGIKREDSRGS~~LIP~~-EGATGFPDQGN~~TGEN~~-----TRQS
 HC1 KDVLNSIA~~AFSS~~-----IAISTVNHADSRASLASLDNPNSTNEKSSEKTDNCEKI~~PRPL~~
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFL~~LT~~STSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSS~~LPY~~KQYN-----

5.1/5.2

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISED~~TL~~LYWN-KVSPQELINILILLEVCL
 HC1 ALIGSTLRFDRLDQAE~~TR~~SLLMCF~~LH~~IMKTISYETLIA~~YWQ~~-RAPSPEVSDFFS~~IL~~CVCL
 HC3 -----TFSAESSRSL~~IC~~LLWVLKN-ADETVLQKWFTDLSVLQ~~LN~~RLLDLLYL~~LCV~~
 HC5 -----MLNADT~~TR~~NLMICFLWIMKN-ADQSLIRK~~WI~~ADLPSTQLNRILDLLFICV

HC2A HQFYMGKRYIARNQEGLG--PIVHDRKS-----QTLFVSRNRTGMM
 KIAA HQFYMGKRYIAR-----TGMM
 rat -----
 HC4 FHFRYMGKRNIARVHD~~AW~~LSKHFGIDRKS-----QTMPALNRNSGVM
 HC1 QNFRYL~~GKR~~NIIRKIAAF--KFVQSTQ~~NG~~TLKGSNPSCQTSGLLAQ~~NH~~STSRHEG~~HK~~
 HC3 SCFEYK~~GK~~VFERMNSLTFK--KSKDMRAK-----LEEAILGSIGARQEMV
 HC5 LCFEYK~~GK~~QSSDKVSTQVLQ--KSRDV~~KAR~~-----LEEALLRGEGARGEMM

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADI~~FH~~QALLEGNTATEVS
 HC1 QHRSQTL~~PI~~IRGK--NALS~~NPKL~~-----LQMLDN~~MT~~SNSEIDIVHHVDTEAN~~IATEGC~~
 HC3 RRSRGQ~~IF~~ERSPSGS~~AF~~GSQENLRWRKDMTHWRQTEKLDK~~SRAE~~IEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP-----GLNENLRW~~KKE~~QTHWRQANEKLDKTKAELDQ~~EAL~~ISGNLATEAH

6.1/6.2

HC2A LTALD~~TL~~SLFTLAF~~N~~QLLADHGHNPLMKKVFDVYLCFLQKHQSE~~TAL~~KNVFTALRSLIY
 KIAA LTALD~~TL~~SLFTLAF~~N~~QLLADHGHNPLMKKVFDVYLCFLQKHQSE~~TAL~~KNVFTALRSLIY
 rat -----
 HC4 KLSRGHSPLMKKVFDVYLCFLQKHQSE~~MAL~~KNVFTALRSLIY
 HC1 LTVLDTISFFTQC~~FK~~TEFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRA~~FIS~~
 HC3 LTILD~~LV~~SLFTQTHQRCLQCCDCQNSLMKRGFD~~TY~~MLFFQV~~NQ~~SATALKHVFASLRL~~FVC~~
 HC5 LIILDTLEIVVQTVS--VTES--KESILGGV~~LK~~VLLHSMACNQSAVYLQHC~~FAT~~QALVS
 LIILDMQENIIQASS--ALDC--KDSLLGGV~~L~~RVLVNSLNCQSTTYLTHC~~FA~~ILRALIA

HC2A KFPSTFYEGRADMC~~AAL~~CYEILKCCNSKLSSIRTEASQLLYFILMRN~~NF~~DYTGKKSFVRTH
 KIAA KFPSTFYEGRADMC~~AAL~~CYEILKCCNSKLSSIRTEASQLLYFILMRN~~NF~~DYTGKKSFVRTH
 rat KFPSTFYEGRADMC~~AS~~LCYEVLKCCNSKLSSIRTEASQLLYFILMRN~~NF~~DYTGKKSFVRTH
 HC4 KFPSAFFKGRVNMCA~~AF~~CYEVLKCC~~TS~~KISSTRNEASALLYLMRN~~NF~~EYTKRKTFLRTH
 HC1 KFPSAFFQGPADLC~~GS~~FCYEVLKCCN~~HR~~SRSTQTEASALLYLMRN~~NF~~EYTKRKTFLRTH
 HC3 KFEPELLFEEETE~~QCAD~~LCLRLLRHCSSSIGTIRSHPSASLYLMRN~~NF~~EYTKRKTFLRTH
 HC5 KFGDLLFEEVE~~QCFD~~LCHQVLHHCSSMDVTRSQACATLYLMRFSFGATS--NFARVK

7.1/7.2

HC2A LQV~~I~~ISVSQ~~LI~~ADVVGIGETR~~FQ~~QSLSIINN~~CAN~~SDRLIKHTSFSSDV~~KDL~~TKRIRT~~VLM~~
 KIAA LQV~~I~~ISVSQ~~LI~~ADVVGIGETR~~FQ~~QSLSIINN~~CAN~~SDRLIKHTSFSSDV~~KDL~~TKRIRT~~VLM~~
 rat LQV~~I~~ISLSQ~~LI~~ADVVGIGETR~~FQ~~QSLSIINN~~CAN~~SDRLIKHTSFSSDV~~KDL~~TKRIRT~~VLM~~
 HC4 LQ~~I~~I~~I~~AVSQ~~LI~~ADVALSGGR~~RFQ~~ESLFIINN~~FAN~~SDRPM~~LAR~~APFAEV~~KDL~~TKRIRT~~VLM~~
 HC1 LQ~~I~~IKAVSQ~~LI~~AD-AGIGGR~~RFQ~~SLAITNNFANGDK~~QMK~~SNFPAEV~~KDL~~TKRIRT~~VLM~~
 HC3 MQVPM~~SL~~SSLVGT~~SQ~~NFNEEFLRRSLRTILTYAEDLELRETTFPDQV~~QDL~~VFNLMILS
 HC5 MQVTMSLASLVGRAPDFNEEHLRRSLRTILAYSEEDTAMQ~~MT~~PFPTQVEELL~~CN~~LSILY

Refs

	Transmembrane
HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGLSEAAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGLSEAAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKTWLD SMARIHVKNGLSEAAAMCYVHV
HC4	ATAQMKEHEKDP EMLID LQYSLAKSYASTPELRKTWLD SMARIHVKNGLSEAAAMCYVHV
HC1	ATAQMKEHEKDP EMLID LQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAAMCYIHI
HC3	DTVKMKEHQEDPEMLID LMYRIAKGYQTS PDLRLTWLQNMAGKHSERSN HAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMD LMYRIAKSYQAS PDLRLTWLQNM AEKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYITRKGV		FRQGCTAFRUITPN
KIAA	TALVAEYITRKEA	VOWEPPLLPHSHSACLRRSRGGVFRQGCTAFRUITPN	
rat	TALVAEYITRKEAD	LALQREPPVFPYSHTSCQRKSRGGMFRQGCTAFRUITPN	
HC4	AALVAEYITRKKL		FPNGCSAFKKITPN
HC1	AALIAEYITRKGYNKVEKICTASLISEDTHPCDSNSLLTTPSGGSMFSGMGPFLSITPN		
HC3	AALVAEYITSMLED		RKYLPGVCVTFFONISSN
HC5	AALVAEYITSMLED		HSYLPVGSVSFONISSN

8.1/8.2

	ITAM
HC2A	IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----VHFNEDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEAGMKEDAGMMD-----VHYSEEVLLLELLEQCVNGLWKAERYETISEISKLI GPI
HC1	IKKEGAAKEDSGMHD-----TPYNE NILVEQLYMCGEFLWKSEYELIADVNKPI IAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASF MAGMYEAVNEVYKVL IPI
HC5	VLEESVSED T LSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVL IPI

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRD FERLAHL YDTIHRAYSKVTEVMHSGRRLLGT YFRVAFFGQAAYQFTDSETDVE			
rat	SMKSGGTLETTHLYDTIHRAYSKVTEVITR-----A-----AGSWDLLPGGLFGQ			
HC4	YENRREFENLTQVYRTIHGAYTKILEVMHTKKRLG-----TFFRVAFY GQ			
HC1	FEKQDFKLLSDLYDYD IHRSYLKVAEVVNSEKRLFG-----HYFRVAFY GQ			
HC3	HEANRDAKKLSTIHGKLQEA FSKIVHSTGWERMFG-----TYFRVGFY G-			
HC5	LEAHREFRKLTLTHSKLQRAFD SIVNKDH--KRMPG-----TYFRVGFY G-			

9.1

	ITAM	ITAM
HC2A	-FFEDEDGKYYIYKEPKLTPLSEISQRL LKIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
KIAA	GFFEDEDGKYYIYKEPKLTPLSEISQRL LKIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
rat	GFFEDEDGKYYIYKEPKLTPLSEISQRL LKIYSDRFGSENVKMIQDSGKVNPKDLDSHYA	
HC4	SFFEEDGKYYIYKEPKLTGLSEISLRLVKIYGERFGTENVKI IQDSKVNKELDPHYA	
HC1	GFFEEDGKYYIYKEPKLTGLSEISQRL LKIYADRFGADNVKI IQDSKVNKELDPHYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRL EGEYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRL EAFYGGCFGAEFVEVIKDSNPVDKCKLDPNKA	

10.1/10.2

	ITAM
HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQKRRITLTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQKRRITLTA
rat	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQKRRITLTA
HC4	HIQVTVKPYFDDKELTERKTEFERMHNISR FVFEAPYTLGKKQGCIEEQKRRITLTT
HC1	YIQVTVYVPFFEEKEIEDRKTDFEMHNNIRRFVETPFTLSGKKHGGVAEQKRRITLTT
HC3	YIQITVVEPYFDYEMKDRITYFDKNYNLRRFMYCTPFTLDGRAHGE LHEQFKRRTILTT
HC5	YIQITVVEPYFDEYEMKDRVTYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT

Coiled-Coil 1

HC2A	IHCFFPVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
KIAA	IHCFFPVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELRQLC	SSAEVDMIKLQLKLQGSV
rat	IHCFFPVKKRIPV	MYQHHTDLN	IEVAIDEMSKKVAELHQLC	SSAEVDMIKLQLKLQGSV
HC4	SNSFPYVKKRIP	INCEQQINLKEIDGATDEIKDKTAE	LQKLCSSSTDVD	MIQLQLKLQGSV
HC1	SHLFPYVKKRIQ	VISQSSTELN	IEVAIDEMSRKVSELNQLCTMEEVDMISLQLKLQGSV	
HC3	SHAFPIKTRVNV	THKEEIIILTRIEVAIEDM	QKKTOELAFATHQDPADPKMLQ	MLVQGSV
HC5	MHAFPIKTRISVI	QKEEFVLTRIEVAIEDM	KKKTLQLAVAINQEP	PPDAKMLQMLVQGSV

Coiled-Coil 2

HC2A	SVQVNAGPLAYARA	FLDDTNTKRYPDNKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
KIAA	SVQVNAGPLAYARA	FLDDTNTKRYPDNKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
rat	SVQVNAGPLAYARA	FLDDTNTKRYPDNKVKLLKEVFRQFVEACGQ	LAVNERLIKEDQLE
HC4	SVQVNAGPLAYARA	FLNDSQASKYPKKVSELKDMFRKFIQACSI	LALELNERLIKEDQVE
HC1	SVKVNAGPMAYARA	FLLEETNAKKYPDNQVKLLKEIFRQFADACGQ	ALDVNERLIKEDQLE
HC3	GTTVNQGPLEVAQ	VFLSEIPSDPKLFRHHNKLRLCFKDFTKRCEDALRKNKSLIGPVQKE	
HC5	GATVNQGPLEVAQ	VFLAEIPADPKLYRHHNKLRLCFKEFIMRCGEA	VEKNKRLITADQRE

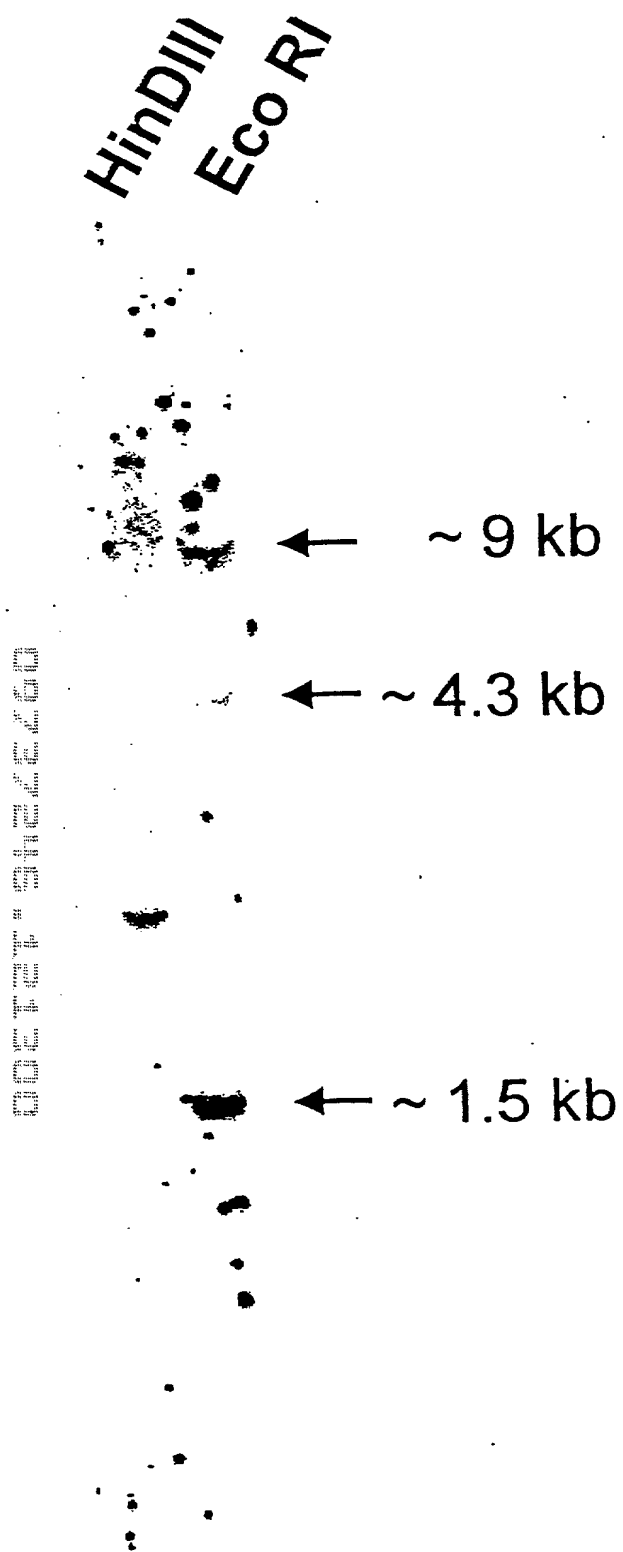
Coiled-Coil 2

HC2A	YQEEKANYREMAKELSEIMHE	QICPLEEKTS-VLPNSLHIFNAISGTP	TSTMVHGMTSS
KIAA	YQEEKANYREMAKELSEIMHE	QLG-----	
rat	YQEEKANYREIRKELSDI	IVERICPGEDKRA	KFPAPHLQRHORDTNKHSGSRVDQF
HC4	YHEGLKSNFRDMVKELSDI	IHEQILOEDTMHSPWMSNTLHVFC	AIISGTSSDRGYGSPRYA
HC1	YQEELRSHYKDMSELSTVM	NEQITGRDDL	SK---RGVDQTC
HC3	YQRELG---	KLSS---	PZ-----
HC5	YQELKKVYNKLNLRPMIE	KIPELYKPIFRVESQKRDSFHRSSFRKC	ETQLSQGSZ-

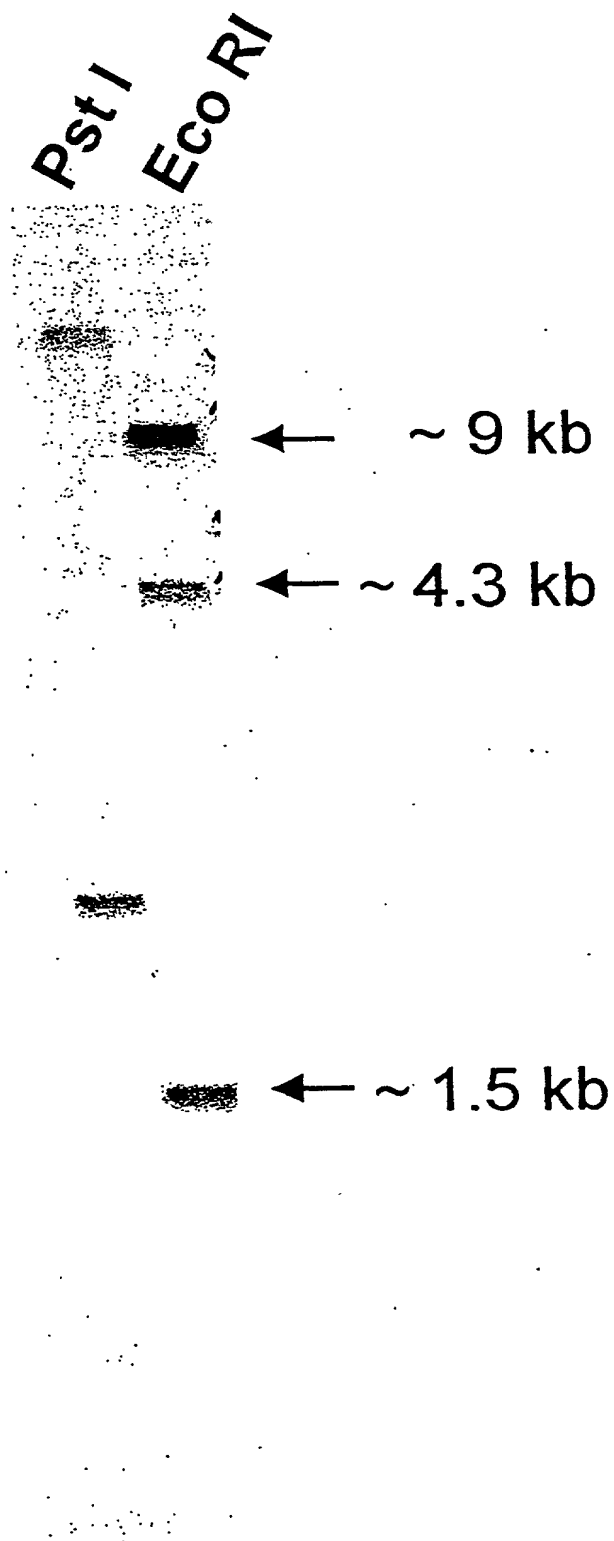
PBM

HC2A	SSVVZ-----
KIAA	-----
rat	CVTLPHEPHVGT
HC4	CFVMCKLRTTFRANHWFCQAQEEAMGN
HC1	GREKEPWTVI
HC3	FNSRFYRSWGK
HC5	EVZ-----
	SAEVZ-----

HC2A	-----
KIAA	-----
rat	VHIFF
HC4	-----
HC1	-----
HC3	-----
HC5	-----



genomic DNA



BAC 9 DNA

FIG. 5

1/1	ATG	GCC	GAG	CGC	CGC	GCC	TTC	GCC	CAG	AAG	ATC	AGC	AGA	ACG	GTG	GCA	GCC	GAA	GTT	AGG
Met	ala	glu	arg	arg	ala	phe	ala	gln	lys	ile	ser	arg	thr	val	ala	ala	glu	val	arg	
61/21										91/31										
AAG	CAG	ATC	TCC	GGA	CAA	TAT	AGT	GGT	TCT	CCC	CAA	CTG	CTC	AAA	AAC	CTT	AAT	ATT	GTT	
lys	gln	ile	ser	gly	gln	tyr	ser	gly	ser	pro	gln	leu	leu	lys	asn	leu	asn	ile	val	
121/41										151/51										
GGC	AAT	ATA	TCC	CAT	CAC	ACC	ACA	GTG	CCC	CTT	ACC	GAA	GCA	GTA	GAT	CCA	GTG	GAT	TTG	
gly	asn	ile	ser	his	his	thr	thr	val	pro	leu	thr	glu	ala	val	asp	pro	val	asp	leu	
181/61										211/71										
GAA	GAT	TAC	CTC	ATT	ACT	CAT	CCT	TTG	GCT	GTG	GAT	TCT	GGG	CCT	TTA	CGG	GAT	TTG	ATT	
glu	asp	tyr	leu	ile	thr	his	pro	leu	ala	val	asp	ser	gly	pro	leu	arg	asp	leu	ile	
241/81										271/91										
GAA	TTT	CCT	CCA	GAT	GAT	ATT	GAA	GTT	GTT	TAT	AGT	CCT	CGG	GAC	TGC	AGA	ACT	CTT	GTT	
glu	phe	pro	pro	asp	asp	ile	glu	val	val	tyr	ser	pro	arg	asp	cys	arg	thr	leu	val	
301/101										331/111										
TCA	GCT	GTA	CCT	GAA	GAA	AGT	GAA	ATG	GAT	CCA	CAT	GTT	AGA	GAC	TGT	ATA	AGA	AGT	TAT	
ser	ala	val	pro	glu	glu	ser	glu	met	asp	pro	his	val	arg	asp	cys	ile	arg	ser	tyr	
361/121										391/131										
ACA	GAA	GAC	TGG	GCA	ATT	GTC	ATC	AGA	AAA	TAT	CAT	AAA	TTG	GGA	ACA	GGA	TTT	AAT	CCC	
thr	glu	asp	trp	ala	ile	val	ile	arg	lys	tyr	his	lys	leu	gly	thr	gly	phe	asn	pro	
421/141										451/151										
AAT	ACA	TTA	GAT	AAA	CAG	AAA	GAA	AGG	CAA	AAA	GGT	TTG	CCA	AAA	CAA	GTT	TTT	GAA	TCT	
asn	thr	leu	asp	lys	gln	lys	glu	arg	gln	lys	gly	leu	pro	lys	gln	val	phe	glu	ser	
481/161										511/171										
GAT	GAA	GCT	CCA	GAT	GGC	AAC	AGC	TAC	CAG	GAT	GAT	CAA	GAT	GAC	CTT	AAA	AGA	CGT	TCA	
asp	glu	ala	pro	asp	gly	asn	ser	tyr	gln	asp	asp	gln	asp	asp	leu	lys	arg	arg	ser	
541/181										571/191										
ATG	TCA	ATA	GAT	GAT	ACC	CCA	AGG	GGT	AGC	TGG	GCC	TGT	AGT	ATC	TTT	GAC	TTG	AAA	AAT	
met	ser	ile	asp	asp	thr	pro	arg	gly	ser	trp	ala	cys	ser	ile	phe	asp	leu	lys	asn	
601/201										631/211										
TCA	CTT	CCT	GAT	GCT	TTG	CTT	CCC	AAT	TTA	CTT	GAT	CGA	ACT	CCA	AAT	GAA	GAA	ATA	GAC	
ser	leu	pro	asp	ala	leu	leu	pro	asn	leu	leu	asp	arg	thr	pro	asn	glu	glu	ile	asp	

1021/341
TTT CTT GTA ATA AAG CTA GAA AAA GTC CTA
phe leu val ile lys leu glu lys val leu

1081/361
CCA TAT ATG ATT TTC AAA GAA GCA GAT GCC
pro tyr met ile phe lys glu ala asp ala

1141/381
AAG AGT CAA GCA GAT CAG TTT TGC CAA AGA
lys ser gln ala asp gln phe cys gln arg

1201/401
ACT GCA ATC CAT TTA ATG AAT ATT GTT AGC
thr ala ile his leu met asn ile val ser

1261/421
GAA GTA GAA ATC AGT ACT GGA GAA CGA AAA
glu val glu ile ser thr gly glu arg lys

1321/441
ATT GTT GGC AGA CGA TCA CTT GAA AGG ACA
ile val gly arg arg ser leu glu arg thr

1381/461
AGC TTT CGA CCA GCT ACT CTC ACA GTG ACA
ser phe arg pro ala thr leu thr val thr

1441/481
AGT GAT GAA GAT CTC TAC AAA TTC CTT GCT
ser asp glu asp leu tyr lys phe leu ala

1501/501
CGA CTA AGA CCT ATT ACA GCT CAG CTC AAG
arg leu arg pro ile thr ala gln leu lys

1561/521
CAT TAT TGC CTA ACT CCG GAG CTG CTT CAA
his tyr cys leu thr pro glu leu leu gln

1621/541
CCT ACC AGA GAA ATC TTA GAG TTT CCC GCA
pro thr arg glu ile leu glu phe pro ala

1681/561
AGA AAT CTT CTC TAC ATA TAC CCT CAG AGT
arg asn leu leu tyr ile tyr pro gln ser

1741/581
AGA AAT ATA ACA GTG AAA GTC CAG TTT ATG
arg asn ile thr val lys val gln phe met

1801/601
GTA ATC TTT GGT AAA TCT AGC TGT TCA GAA
val ile phe gly lys ser ser cys ser glu

1861/621
TAT CAT AAC AGG TCT CCT GAT TTT CAT GAA
tyr his asn arg ser pro asp phe his glu

1921/641
ACT GAC CAT CAT CAC TTG CTT TTT ACT TTT
thr asp his his his leu leu phe thr phe

1981/661
ACT CCT CTT GAA ACA CCA GTT GGA TAT ACA
thr pro leu glu thr pro val gly tyr thr

2041/681
AAG ACT GGC CAG TTT TGC TTG CCA GTC TCA
lys thr gly gln phe cys leu pro val ser

2101/701
CTG TCT CCT GAG GTT CCT CTA CCT GGC ATG
leu ser pro glu val pro leu pro gly met

1051/351
CAG CAA GGA GAC ATT GGA GAG TGT GCA GAA
gln gln gly asp ile gly glu cys ala glu

1111/371
ACC AAG AAT AAA GAA AAA CTG GAG AAA CTG
thr lys asn lys glu lys leu glu lys leu

1171/391
CTT GGG AAA TAT CGC ATG CCT TTT GCT TGG
leu gly lys tyr arg met pro phe ala trp

1231/411
AGT GCT GGG AGT TTG GAA AGA GAT TCT ACA
ser ala gly ser leu glu arg asp ser thr

1291/431
GGG TCT TGG TCA GAG AGG AGG AAT TCT AGT
gly ser trp ser glu arg arg asn ser ser

1351/451
ACA AGT GGA GAT GAT GCT TGT AAC TTG ACG
thr ser gly asp asp ala cys asn leu thr

1411/471
AAT TTT TTT AAG CAG GAA GGA GAC CGC TTA
asn phe phe lys gln glu gly asp arg leu

1471/491
GAT ATG AGA AGG CCA TCT TCT GTC TTA CGG
asp met arg arg pro ser ser val leu arg

1531/511
ATA GAC ATT TCT CCC GCA CCT GAA AAT CCC
ile asp ile ser pro ala pro glu asn pro

1591/531
GTG AAG CTT TAC CCT GAC AGT AGA GTT AGA
val lys leu tyr pro asp ser arg val arg

1651/551
AGG GAT GTT TAT GTT CCA AAC ACT ACT TAC
arg asp val tyr val pro asn thr thr tyr

1711/571
CTT AAT TTT GCC AAT CGT CAA GGT TCT GCT
leu asn phe ala asn arg gln gly ser ala

1771/591
TAT GGA GAG GAT CCA AGC AAT GCC ATG CCG
tyr gly glu asp pro ser asn ala met pro

1831/611
TTT TCA AAG GAA GCC TAT ACA GCC GTA GTA
phe ser lys glu ala tyr thr ala val val

1891/631
GAA ATC AAG GTT AAG CTT CCT GCT ACT TTA
glu ile lys val lys leu pro ala thr leu

1951/651
TAT CAT GTT AGT TGT CAA CAA AAA CAA AAT
tyr his val ser cys gln gln lys gln asn

2011/671
TGG ATA CCA ATG CTT CAG AAT GGA CGG TTG
trp ile pro met leu gln asn gly arg leu

2071/691
TTG GAA AAA CCA CCA CAG GCT TAT TCT GTA
leu glu lys pro pro gln ala tyr ser val

2131/711
AAA TGG GTA GAT AAT CAC AAA GGT GTT TTT
lys trp val asp asn his lys gly val phe

3301/1101	GTG TCT TCA AAG CTT TAC TCA TTA CCG AAT	3331/1111	CCC AGT GTT CTG GTG TCC TTG AGG CTG GAT
val ser ser lys leu tyr ser leu pro asn	pro ser val leu val ser leu arg leu asp	3391/1131	TAT GTT ACA TTA AAC TTA CCC TGC AGC TTA
3361/1121	TTT CTA CGA ATC ATC TGC AGT CAT GAG CAC	3421/1141	phe leu arg ile ile cys ser his glu his
3421/1141	CTT ACT CCA CCT GCA TCT CCA TCA CCT TCT	3451/1151	GTT TCT TCT GCA ACA TCT CAG AGT TCT GGA
3481/1161	leu thr pro pro ala ser pro ser pro ser	3511/1171	val ser ser ala thr ser gln ser ser gly
3541/1181	TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	3571/1191	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
3601/1201	phe ser thr asn val gln asp gln lys ile	3631/1211	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
3661/1221	CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	3691/1231	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
3721/1241	arg gln gln his tyr leu ala gly leu val	3751/1251	lys val ile asn met val his asn leu leu
3781/1261	GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	3811/1271	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
3841/1281	asp ala glu gly leu phe gly leu his lys	3871/1291	asp pro gln ile lys ala arg val ala met
3901/1301	TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	3931/1311	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
3961/1321	leu thr arg pro gly ser phe leu leu thr	3991/1331	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
4021/1341	TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC	4051/1351	cys ile ala thr asp asp tyr glu ser glu
4081/1361	GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT	4111/1371	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
4141/1381	ser gly ser met ile ser gln thr val ala	4171/1391	met ala ile ala gly thr ser val pro gln
4201/1401	CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	4231/1411	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
4261/1421	leu thr arg pro gly ser phe leu leu thr	4291/1431	GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT
4321/1441	ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA	4351/1451	GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
4381/1461	met asn ser leu thr phe lys lys ser lys	4411/1471	GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
4441/1481	CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG	4501/1501	GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
4501/1501	leu gly ser ile gly ala arg gln glu met	4561/1521	val arg arg ser arg gly gln leu glu arg
4561/1521	AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA	4621/1541	GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
4621/1541	ser pro ser gly ser ala phe gly ser gln	4681/1561	AAA TCA AGA GCA GAG ATT GAA CAC GAA GCA
4681/1561	CAC TGG CGT CAA AAC ACA GAG AAG CTT GAC	4741/1581	lys ser arg ala glu ile glu his glu ala
4741/1581	his trp arg gln asn thr glu lys leu asp	4801/1601	CTG ATT GAT GGA AAC CTG GCT ACA GAA GCA
4801/1601	leu ile asp gly asn leu ala thr glu ala	4861/1621	AAC CTA ATC ATT TTA GAT ACA TTA GAG ATT
4861/1621	leu thr arg pro pro ala ser pro ser pro ser	4921/1641	val ser ser ala thr ser gln ser ser gly
4921/1641	TTT TCT ACG AAT GTA CAA GAC CAA AAG ATT	4981/1661	GCA AAT ATG TTT GAA TTA TCC GTG CCT TTC
5001/1681	phe ser thr asn val gln asp gln lys ile	5041/1681	TTA ACA GAG CTG GCT GTC ATT TTA GAC CCT
5041/1681	CGC CAA CAG CAT TAT TTG GCA GGA CTT GTG	5101/1701	leu thr glu leu ala val ile leu asp pro
5101/1701	arg gln gln his tyr leu ala gly leu val	5161/1721	AAA GTC ATC AAT ATG GTA CAC AAT TTA CTC
5161/1721	GAT GCT GAA GGA CTG TTT GGA TTG CAT AAG	5221/1741	lys val ile asn met val his asn leu leu
5221/1741	asp ala glu gly leu phe gly leu his lys	5281/1761	GAC CCT CAG ATA AAG GCT CGA GTG GCC ATG
5281/1761	TCC AGT CAC GAC TCA GAC CCG CGG TAC TCT	5341/1781	asp pro gln ile lys ala arg val ala met
5341/1781	ser ser his asp ser asp pro arg tyr ser	5401/1801	GAA ACT GTA CCT CAG CTG TAT GAT TTT ACA
5401/1801	TTG TAT CTA CCT CTG ATT GGT ATT ATC ATG	5461/1821	glu thr val pro gln leu tyr asp phe thr
5461/1821	leu tyr leu pro leu ile gly ile ile met	5521/1841	TGT ATA GCC ACT GAT GAT TAT GAA AGT GAG
5521/1841	GAA ACT CAC AAT CAA CGA GGA AGA CCA ATT	5581/1861	cys ile ala thr asp asp tyr glu ser glu
5581/1861	glu thr his asn gln arg gly arg pro ile	5641/1881	ATG GCA ATC GCA GGG ACA TCG GTC CCT CAA
5641/1881	AGC GGA AGT ATG ATA AGC CAG ACC GTT GCC	5701/1901	met ala ile ala gly thr ser val pro gln
5701/1901	ser gly ser met ile ser gln thr val ala	5761/1921	TCA ACG AGT GGC AGG CAA CAC ACT ACC TTT
5761/1921	CTA ACA AGG CCT GGC AGT TTC CTC CTC ACG	5821/1941	leu thr arg pro gly ser phe leu leu thr
5821/1941	leu thr arg pro gly ser phe leu leu thr	5881/1961	TCA GCA GAA TCA AGT CGA AGC CTT TTG ATC
5881/1961	ser ala glu ser ser arg ser leu leu ile	5941/1981	TGT CTA CTT TGG GTT CTC AAA AAT GCA GAT
5941/1981	ser ala glu ser ser arg ser leu leu ile	6001/2001	cys leu leu trp val leu lys asn ala asp
6001/2001	GAA ACA GTT CTA CAG AAG TGG TTT ACA GAT	6061/2021	CTC TCA GTC TTG CAG CTA AAC CGG CTA TTA
6061/2021	glu thr val leu gln lys trp phe thr asp	6121/2041	leu ser val leu gln leu asn arg leu leu
6121/2041	GAT CTG CTT TAT CTC TGT GTG TCT TGC TTT	6181/2061	GAG TAT AAA GGG AAA AAA GTG TTT GAA CGA
6181/2061	asp leu leu tyr leu cys val ser cys phe	6241/2081	glu tyr lys gly lys lys val phe glu arg
6241/2081	ATG AAT AGC TTG ACC TTT AAG AAA TCA AAA	6301/2101	GAC ATG AGA GCA AAG CTT GAA GAA GCT ATT
6301/2101	met asn ser leu thr phe lys lys ser lys	6361/2121	asp met arg ala lys leu glu glu ala ile
6361/2121	CTT GGG AGC ATA GGT GCC AGG CAA GAA ATG	6421/2141	GTA CGG CGA AGC CGA GGA CAG CTC GAG AGA
6421/2141	leu gly ser ile gly ala arg gln glu met	6481/2161	val arg arg ser arg gly gln leu glu arg
6481/2161	AGC CCA TCT GGA AGT GCC TTT GGA AGT CAA	6541/2181	GAA AAT TTG AGG TGG AGG AAA GAT ATG ACT
6541/21			

5581/1861	5611/1871
GCA GAG ATA TCT CAC AGA TTG GAG GGA TTT	TAC GGA GAA AGA TTT GGA GAG GAT GTG GTT
ala glu ile ser his arg leu glu gly phe	tyr gly glu arg phe gly glu asp val val
5641/1881	5671/1891
GAA GTA ATC AAA GAC TCT AAT CCT GTA GAC	AAG TGT AAA TTA GAT CCT AAC AAG GCA TAT
glu val ile lys asp ser asn pro val asp	lys cys lys leu asp pro asn lys ala tyr
5701/1901	5731/1911
ATT CAG ATT ACC TAT GTG GAG CCA TAC TTT	GAC ACA TAT GAG ATG AAG GAC AGA ATC ACC
ile gln ile thr tyr val glu pro tyr phe	asp thr tyr glu met lys asp arg ile thr
5761/1921	5791/1931
TAT TTC GAC AAA AAT TAC AAT CTT CGT CGA	TTC ATG TAC TGT ACA CCC TTT ACT TTA GAT
tyr phe asp lys asn tyr asn leu arg arg	phe met tyr cys thr pro phe thr leu asp
5821/1941	5851/1951
GGC CGT GCC CAT GGG GAA CTT CAT GAA CAA	TTC AAA AGG AAG ACC ATT CTG ACT ACG TCT
gly arg ala his gly glu leu his glu gln	phe lys arg lys thr ile leu thr thr ser
5881/1961	5911/1971
CAT GCC TTT CCT TAT ATT AAA ACA AGG GTC	AAT GTC ACT CAT AAA GAA GAG ATC ATC TTA
his ala phe pro tyr ile lys thr arg val	asn val thr his lys glu glu ile ile leu
5941/1981	5971/1991
ACA CCA ATT GAA GTT GCT ATT GAG GAC ATG	CAG AAA AAG ACA CAG GAG TTG GCA TTT GCA
thr pro ile glu val ala ile glu asp met	gln lys lys thr gln glu leu ala phe ala
6001/2001	6031/2011
ACA CAT CAG GAT CCC GCA GAC CCC AAA ATG	CTT CAG ATG GTA CTC CAG GGA TCT GTA GGC
thr his gln asp pro ala asp pro lys met	leu gln met val leu gln gly ser val gly
6061/2021	6091/2031
ACC ACA GTG AAT CAG GGG CCT TTG GAA GTT	GCC CAG GTT TTT CTG TCT GAA ATA CCT AGT
thr thr val asn gln gly pro leu glu val	ala gln val phe leu ser glu ile pro ser
6121/2041	6151/2051
GAC CCA AAG CTC TTC AGA CAT CAT AAT AAA	CTG CGA CTC TGC TTT AAA GAT TTT ACT AAA
asp pro lys leu phe arg his his asn lys	leu arg leu cys phe lys asp phe thr lys
6181/2061	6211/2071
AGG TGT GAA GAT GCC TTA AGA AAA AAT AAG	AGC TTA ATT GGG CCG GTT CAA AAG GAG TAT
arg cys glu asp ala leu arg lys asn lys	ser leu ile gly pro val gln lys glu tyr
6241/2081	6271/2091
CAA AGG GAA TTG GGG AAA CTA TCT TCG CCT TAA	
gln arg glu leu gly lys leu ser ser pro OCH	

AGAGGCCCTACAGCCCTAGATCACAGAAAGTCCCTCAGTTATCCAAGCCAGTATTGCTTGTCCCCTGCCACAGAGATTCC
TTCAGTCGAATGAGCTTTTCGCAAAATGGATCTCTAAACTGAATGCACTTGTTTTATTTCATCTGCAAAGAGCCATGTATTC
AACATCGAGTGTGAAAAGATCTATTGGAAACCAACATGGAATGGAATTCTGGAAATTATTATTCAATTGAAGAATGCAGTG
GCCAAGAAAATATCAAATGTAGATTGTTAACGCTTGAGAATCATGGCTATGGTTTCTAATGTTTCGGGTAACAAGCTGTTA
TCTTTTAAGACATTTTAATGACTCAAAGGTACACTATACATTTACCATTATTTATACCATAGCTAAGGTTAAAAATTTAT
TCACTTTAAGTTTCGTATTTTTTAATTTATATCACCATTATAGATTCATTTTGGACCCATTTTAAATGTAGTAATGCTTA
TTTTAAAGGTACTAAAAAATATGTGAATGTTTACCTCGTGCGCGCCAGGGCCTC

A. Allelic Variations: single nucleotide changes (polymorphisms) between hCLASP-3 cDNAs and/or genomic sequences

Isoform	Difference	Nucleotide position	Consequence
1	polymorphism	318	A to G; missense
2	polymorphism	323	A to G; Glu to Gly
3	polymorphism	2187	T to C; missense
4	polymorphism	3165	T to G; Asp to Glu

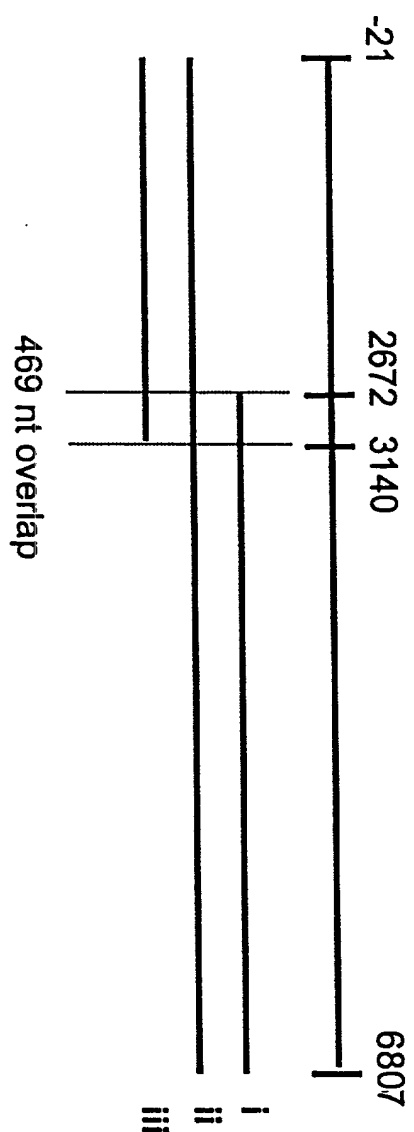
B. Alternative Exon usage

Isoform	Difference	Nucleotide position	Consequence
1	Exon deletion	2768-2860, inclusive	In frame deletion – 33 amino acids removed

These differences may be found separately or together in various combinations in the different human CLASP-3 isoforms

FIG. 6

nucleotide numbering
as in Figure 6A



C

[illegible]

Exon 60270 - 20370

CGCCGCAGCCGCCGCCGCCGTCGCCGTCGCCGCAGCAGCCATGGCCGAGCGC
CGCGCCTTCGCCCAGAAGATCAGCAGGTAAATATCCGGCGTGGGGCGC

Exon 85360 - 85510

GTTTTTGCTTTCTTCATTGTAGAACGGTGGCAGCCGAAGTTAGGAAGCAGATC
TCCGGACAATATAGTGGTTCTCCCCAACTGCTCAAAAACCTTAATATTGTTGG
CAATATATCCCATCACACCACAGTAAGTAACGTATTCAAAATATA

Exon 94500 - 94720

TCTTATCCCAACTTTTTTACAAAGGTGCCCTTACCGAAGCAGTAGATCCAGTG
GATTTGGAAGATTACCTCATTACTCATCCTTTGGCTGTGGATTCTGGGCCTTT
ACGGGATTTGATTGAATTTCTCCAGATGATATTGAAGTTGTTTATAGTCCTC
GGGACTGCAGAACTCTTGTTTCAGCTGTACCTGAAGAAAGGTAAGGAGACAT
TGACTTATT

Exon 94870 - 94980

TATTTTCCTTTTTTAAAATAGTGAAATGGATCCACATGTTAGAGACTGTATAAG
AAGTTATACAGAAGACTGGGCAATTGTCATCAGAAAGTAAGTTATATGTTTA
TTACAA

Exon 100110 - 100290

ATTTATTTAACCTTTTTTTCTTTAATAGATATCATAAATTGGGAACAGGATTTAA
TCCCAATACATTAGATAAACAGAAAGAAAGGCAAAAAGGTTTGCCAAAACA
AGTTTTTGAATCTGATGAAGCTCCAGATGGCAACAGCTACCAGGATGATCAA
GTAATACTTTTATTCTTAAATAA

Exon 100340 - 100600

ATATTTAATGTTTTGCATGACAGGATGACCTTAAAAGACGTTCAATGTCAATA
GATGATACCCCAAGGGGTAGCTGGGCCTGTAGTATCTTTGACTTGAAAAATT
CACTTCCTGATGCTTTGCTTCCCAATTTACTTGATCGAACTCCAAATGAAGAA
ATAGACCGTCAGAAATGATGACCAAAGGAAATCAAACCGTCACAAAGAACCTT
TTGCTTTGCATCCATCACCAGATGAGGTATAGATGTTTGCATATAAAGAA

Exon 100880-101020

TTTTGGTGTGCTTTTCAATTTGTAGGAAGAACCAATAGAACGGCTTAGTGTT
CCTGATATACCCAAAGAACATTTTGGTCAAAGACTTCTTGTA AAAATGCTTATC
ACTCAAGTGAGTATTTATTTCTTTTACTTACAAC

Exon 112010 – 112120

TTTTTCTTCATAAAGGTTTGAAATTGAAATTGAACCCATTTTGTCAAGTTTGG
CTTTATATGATGTCAAGGAAAAGAAAAAGGTAAGATTATATAATTTGACCAT
AGTTAT

Exon 113680 – 113880

AAGTTTAACATACTAATATTTTTTTAGATTTTCAGAAAACTTTTATTTTGACCTTA
ATTCTGAGCAGATGAAAGGGTTGTTACGTCCACATGTACCACCTGCTGCCATT
ACTACCCTGGCAAGATCAGCAATTTTTTCTATCACTTATCCTTCCCAAGATGT
TTTTCTTGTAATAAAGGTGAGAATAATGTTAAATATATTTG

Exon 115020-115160

TTAATCTTAACTTTTTTTGCCTTTGACAGCTAGAAAAAGTCCTACAGCAAGGA
GACATTGGAGAGTGTGCAGAACCATATATGATTTTCAAAGAAGCAGATGCCA
CCAAGGTAGAATGTTATGCTTCTCATTTCGCCAC

Exon 117200 – 117410

ATGTATAAAGTTCTGTTTTGCAGAATAAAGAAAACTGGAGAACTGAAGAG
TCAAGCAGATCAGTTTTGCCAAAGACTTGGGAAATATCGCATGCCTTTTGCTT
GGACTGCAATCCATTTAATGAATATTGTTAGCAGTGCTGGGAGTTTGGAAG
AGATTCTACAGAAGTAGAAATCAGTACTGGAGGTAAGAGTGTTTCATACAAA
AC

Exon 123200 - 123396

AAAATGAATTTTTTTTTTAATTCTTTGTAGAACGAAAAGGGTCTTGGTCAGA
GAGGAGGAATTCTAGTATIGTTGGCAGACGATCACTTGAAAGGACAACAAGT
GGAGATGATGCTTGTAACCTTGACGAGCTTTCGACCAGCTACTCTCACAGTGAC
AAATTTTTTAAGCAGGTATTGTTCTGTCATGTAGGAATTTT

(Next part of CLASP, starting

GAAGGAGACCGCTTAAGTGATGAAGATCTCTACAAATTCCTTGCTGATATGA
GAAGGCCATCTTCTGTCTTACGGCGACTAAGACCTATTACAG)

Exon 5560 – 5710

CTTTTTCCTCTATTATTGAAATCAGGAAGGAGACCGCTTAAGTGATGAAGATC
TCTACAAATTCCTTGCTGATATGAGAAGGCCATCTTCTGTCTTACGGCGACTA
AGACCTATTACAGGTATTTAAAAATTTGAGTAGAAATGGTTGCA

Exon 6680-6900

TTACATTGTTTTTTAATATATAATTTGCAGCTCAGCTCAAGATAGACATTTCTC
CCGCACCTGAAAATCCCCATTATTGCCTAACTCCGGAGCTGCTTCAAGTGAA
GCTTTACCCTGACAGTAGAGTTAGACCTACCAGAGAAATCTTAGAGTTTCCCG
CAAGGGATGTTTATGTTCCAAACACTACTTACAGGTAAGAGATTTTAATTGG
AGAATTCTG

Exon 38920 – 39075

GTATTTACTATCATCTATACTGTTGCTTTCACAGAAATCTTCTCTACATATACC
CTCAGAGTCTTAATTTTGCCAATCGTCAAGGTTCTGCTAGAAATATAACAGTG
AAAGTCCAGTTTATGTATGGAGAGGATCCAAGCAATGCCATGCCGGTAA


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hCLASP4 -----MFPMEDISISVIGRQRRTVQ----- 20
hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLNINIVG 41
hCLASP2 -----MLLFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFVKREPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLEPLDYETVIEELEKTYRN 60
      .
      .
      .

hCLASP4 -----STVPEDAQKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
hCLASP2 -----TVPKAEQSLFVTECIKTYNSDWHLVNYK 55
hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
hCLASP1 DPLQDLLFFPSDDFSAATVSWDIRTLYSTVPEDAHEKAENLLVKEACKFYSSQWHVVNYK 120
      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQPSLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFRQLPNKVVKLDKLPVHVYEVDEEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADDLELLLQPRECRTEP-GIPKD-EKLDQAQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSHSFEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
      :: .      : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKROKQ-LPKQVFESDEAPDGNYSYQDDQDDLKRRSMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQRERQKG-LPRQVFQDASGDERSGPEDSNDSSRRSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSC 239
      : :      . : : * : : . : .

hCLASP4 DVVQCPKMRRAFAELKMLDKYSHYLAAETEQEEMEWLITLKKIIQINTDSLVOEKKETVE 222
hCLASP5 DVSGKGPTACDFDLRSLQDPKRLNLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRQNDQKRSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSYLLAADSEVEMEEWITILNKILQLN-----FEAMQEK 219
hCLASP7 EDTPRSSGASSIFDLRNLAADSLPSLLERAAPEDVDRRNETLRRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNLDLTYFVLAATESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : :      . : : . : :

hCLASP4 TAQDDDETSS----QGKAENIMASLERSMHPELMKYGRETEQLNKLSRGDGRQNLFSFDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPECPKEHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEPIERLSVPDIPKEHFG-----QRLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLDSYLPPELAKSAREAEIK---LKSESRVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRLVKCLSLKFEIE 273
hCLASP1 TDLGLDSLNSVTCECTPEETDSSNNLHADFAKYLTETEDTVKTTNRMERLNLFSLDPD 359
      .      :      :      : : : : : : :

hCLASP4 VQRLDFS----GIEPDIKP-FEEKCNKRLVFNCHDLTFNILGQIGDNAKGPPPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKI SENFHC DLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKI SENFYFDLNSQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDIFS----SAEPEVKS-FEEKFGKRILVKCNLDSFNLQCCVAENEEGPTTNVEPFFV 327
hCLASP7 IEPIFGI----LALYDVREKKI SENFYFDLNSDSMKGLLRAGHTPAISTLARSAIFSV 329
hCLASP1 IDTLKLQKKDLLEPESVIKPFEEKA AKRIMIICKALNSNLQGCVTENENDPITNIEPFFV 419
      : :      . : : . : : . : : * :

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hCLASP4	hCLASP5	hCLASP3	hCLASP2	hCLASP7	hCLASP1	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713
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hCLASP4	FKSHLESTIYTQDLHVHKFFHHCQLIQS-----GSKEVPGELIKYLKCLHAM	794
hCLASP5	IEVQAVSSVHTQDNHLEKFFTLCHSLESQVTFPIRVLDQKISEMALEHELKLSIICLNSS	715
hCLASP3	VEVVAVSSIHTQDPYLDKFFALVNALDEH-LFPVRIGDMRIMENNLLENELKSSISALNSS	780
hCLASP2	ISTHLVSTVYTQDQHLHNFFQYCKTES-----GAQALGNELVKYLKSLHAM	787
hCLASP7	VELTAVSSVHPQDPYLDKFFTLVHVLEEG-AFPFRLKDTVLSSEGNEQELRASLAALRLA	767
hCLASP1	VSTFVVSTVNTQDPHVNAFFQECQKREK-----MSQSPTS NFIRSCKNLLNVE	887
	.. *:: ** ::. ** : :.	
hCLASP4	EDQVMIQFLPVILMQLER-----VLTNMT-----EDDVP	824
hCLASP5	RLEPLVLFLHLVLDKLFQLSVQPMVIAGQTANFSQFAFESVVAIANSLHNSKDLSDQH	775
hCLASP3	QLEPVVRFLHLLLDKLIILLVIRPPVIAGQIVNLGQASFEAMASINRLHKNLEGNHDQH	840
hCLASP2	EGHVMIAFLPTILNQLER-----VLT-RAT-----QEEVA	816
hCLASP7	SPEPLVAFSHHVLDKLVRLVIRPPIISGQIVNLGRGAFFAMAHVVSILVHRSLEAAQDARG	827
hCLASP1	KIHAIMSFLPIILNQLER-----VLVQNE-----EDEIT	916
	. :: * : * : *	
hCLASP4	INCTMV-LLHIVSKCHEEGLDS-----YLRSEFIKYS-----FRPEKP	860
hCLASP5	RNCLLASVYHYVFRLEPVQRDVPKSGAPTALLDPRS YHTYGR TSAAAVSSKLLQARVMSS	835
hCLASP3	RNSLLASYIHVFRLEPNTYPNSSSPG-PGGLGGSVHYATMARSAVRPASLNLNRSRSLN	899
hCLASP2	VNVTRV- I IHVVAQCHEEGLES-----HLRSYVKYA-----YKAEPY	852
hCLASP7	HCPQLAAYVHYAFRLPGTEPSLPDGAPP---VTVQAATLARGSGRPASLYLARSKSIS	883
hCLASP1	TTVTRV-LPDI VAKCHEEQLDH-----SVQSYIKFV-----FKTRAC	952
	. . . :	
hCLASP4	SAPQAQLIH-----ETLATTMIAILKQS-----	883
hCLASP5	SNPDLAGTHSAADEEVKNIMSSKIADRNC SRMSYYCSGSSDAPSSPA-----	882
hCLASP3	SNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSPSPSAESTQAMDRSC	959
hCLASP2	VASEYKTVH-----EELTKSMTTILKPS-----	875
hCLASP7	SNPDLAVAPGSVDDEVSRILASKLLHEELA-LQ-----	915
hCLASP1	KE---RPVH-----EDLAKNVTGLLSKN-----	972
	: . .	
hCLASP4	-----ADFLSINKLLKYS-----WFFFEIIAKSM	907
hCLASP5	-----APRPASKKHFEELALQ-----MNVSTGMVKSM	910
hCLASP3	NRMSSHTETSSFLQTLTGRLP TKLFHEELALQWVVCSGSVRESALQQA WFFFEIMVKSM	1019
hCLASP2	-----ADFLTSNKLLRYS-----WFFFDVLKSM	899
hCLASP7	-----WVVS SAVREAILQHA-----WFFFQLMVKSM	942
hCLASP1	-----DSPTVKHVLKHS-----WFFF AIILKSM	995
	. * .. : ***	
Cadherin Cleavage		
hCLASP4	ATYLLEENKIKLHGRQFPETYHHVLHSLLLAIIPHVTIRYAEIPDE---SRNVNYSLAS	964
hCLASP5	AQHVHNM DKRDSERRTRFSDFRMDDIITIVNVVTSEIAALLVKPQKENEQA EKMNISLAF	970
hCLASP3	VHHLVFNDKLEAHRKSRFPERFMD DIAALVSTIASDIVSRFOKDTEM---VERLNTSLAF	1076
hCLASP2	AQH LIENSKVKLIRNORFPASYHHAETVVNMLMPHITQKFGDNPEA---SKNANHSLAV	956
hCLASP7	ALHLLLGQRLDTERKLRFPGRFLDDITALVGSVGLVITRVHKDVEL---AEHLNLSLAF	999
hCLASP1	AQHLIDTNKIQLERPQRFPESYQNELDNLMVLSDHVIWKYKDALEE---TRRATHSVAR	1052
	. :: . . . * * . . . : : . . . * : *	
hCLASP4	FLKRCLTLMDRGFIFNLINDYISGFSPKDP-----KVLAEYKFEFLQTICNHEHYIPLNL	1019
hCLASP5	FLYDLLSLMDRGFVFNLI RHYSQLSAKLSNL---FTLISMRLFLRILCSHEHYLN LNL	1027
hCLASP3	FLNDLLSVMDRGFVFSLIKSCYKQVSSKLYSLPNPSVLVSLRLD FLRIICSHEHYVT LNL	1136
hCLASP2	FIKRCFTFMDRGFVFKQINNYISCFAPGDP-----KTLFEYKFEFLRVVCNHEHYIPLNL	1011
hCLASP7	FLSDLLSLVDRGFVFSLVRAHYKQVATRLQSSPNPAPALLTLRMEFTRIILCSHEHYVT LNL	1059
hCLASP1	FLKRCFTFMDRGCVFKMVNNYISMFS S GDL-----KTLCOYKFDFLQEVQCHEHFIPCL	1107
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hCLASP4 NNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAF CY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDOSTTYLTHCFATLRALIAKFGDLLFEEVEQCFDLCH 1425
hCLASP3 SKES---ILGGVLKVLHSMACNQSAVYLQHC FATQRALVSKFPPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPLMKKVFDVYLCFLQKHQSE TALKNVFTALRS LIYKFPSTFYEGRADMCAALCY 1431
hCLASP7 ARE---VLGAVLKVVLYSLGSAQSALFLQHGLATQRALVSKFPPELLFEEDTEL CADLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQV NQSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQCACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSQNFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLLYFLMRNFDYTGKKS FVRTHLQVIIISVSQLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGHNFARVKMQVTMSLSSLVGTTQNFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSQLIADAG-IGG 1619
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hCLASP4 SRFOESLFIINNFANS DRPMKATAFPAEVKDLTKRIRTVLMATAQMKHEKDP EMLIDLQ 1539
hCLASP5 EHLRRSLRTILAYSEEDTAMQMTFPPTQVEELL CNLSILYDTVKMREFQEDPEMLMDLM 1543
hCLASP3 EFLRRSLKTI LTYAEEDLELRETTFPDQVDLFNLHMILSDTVKMKEHQEDPEMLIDL M 1664
hCLASP2 TRFQSSLSI INNCANS DRLIKHTSFSSDVKDLTKRIRTVLMATAQMKHEHNDPEMLVDLQ 1551
hCLASP7 EHLRRSLKTI LTYAEEDMGLRDSTFAEQVDLMFNLHMILDTVKMKEHQEDPEMLIDL M 1582
hCLASP1 SRFOHSLAITNNFANGDKQMKNSNFP AEVKDLTKRIRTVLMATAQMKHEKDP EMLVDLQ 1679
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transmembrane

hCLASP4 YSLAKSYASTPELRKTWLD SMAKIHVKNGILFSEAAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNM AEKHTKKQY TEAAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSPE-RLTWLQNMAGKHSERSNHA EAAQCLVHSAALVAEYLSMLED R----- 1718
hCLASP2 YSLAKSYASTPELRKTWLD SMARIHVKNGLLSEAAMCYVHV TALVAEYLTRKG----- 1604
hCLASP7 YRIARGYQGS PDLRLTWLQNMAGKHAELGNHAEAAQCMVHAAALVAEYI ALLEDQ----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGILSEAAMCYIHIAALIAEYIKRKG YWKVEKI 1739
* : : * : : * : : * : : *

hCLASP4 -----LFPNGCSAFKKITPNIDE EGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVS EDTLSPDEG V----- 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVS DDVVPDEEGI----- 1753
hCLASP2 -----VFRQCGTA FRVITPNIDE EASMMEDVGMQD----- 1634
hCLASP7 -----RHLPGCVSFQNISSNVLEESAIS DDILSPDEEGF----- 1672
hCLASP1 CTASLLSE DTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEGA AKEDSGMHD----- 1795
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ITAM

hCLASP4 ---VHYSEEV LLELLEQCVDGLWKAERYEII SEISK LIVPIYEK RREFEKL TQVYRTLHG 1679
hCLASP5 CAGQYFTESGLVGLLEQA AELFSTGGLYETVNEVYKLVIP ILEAHREFRKLTLTHSKLQR 1693
hCLASP3 CSGKYFTESGLVGLLEQA AASFMSMAGMYEAVNEVYKLVIP IHEANRDAKKLSTIHGKIQE 1813
hCLASP2 ---VHFNE DVLME LLEQCADGLWKAERYELIADIYKLIIP IYEKRR----- 1677
hCLASP7 CSGKHFTELGLVGLLEQA AGYFTMGGLYEAVNEVYKNLIP ILEAHRDYKKLA AVHGKIQE 1732
hCLASP1 ---TPYNE NILVEQLYMCGEFLWK SERYELIADVNKPIIAVFEKQRDFKKLS DLYYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM

hCLASP4 AYTKILEVMHTKKRL LGTFFRVAFYQG SFFFEEDGKEYIYKEEKL TGLSEISRLRVKIYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFY G-SKFGDLDEQE FVYKEFAITKLPEISHRLEAFY G 1750
hCLASP3 AFSKI VHQSTGWERMFGTYFRVGFY G-TKFGDLDEQE FVYKEFAITKLAEISHRLEGFY G 1872
hCLASP2 -----DFFEDEGKEYIYKEEKL TPLSEISQRLLK IYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFY G-AHFGDLDEQE FVYKEFSITKLAEISHRLEEFYT 1791
hCLASP1 SYLKVAEVVNSEKRLFG RYRVAFYQG SFFFEEDGKEYIYKEEKL TGLSEISQRLLK IYA 1912
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FIG. 8
5 of 6

ITAM

hCLASP4 EKFGTENVKIIQSDSKVNAKELDPHYAHIQVTVVKKYFDDKELTERKTEFERNHNISRfV 1799

hCLASP5 QCFGAEFVEVIKDSPTVDKTKLDPNKAYIQITEVEYFDEYEMKDRVTYFEKNFNLRfM 1810

hCLASP3 ERFGEDEVVEIKDSNPVDKCKLDPNKAYIQITYVEYFDYEMKDRITYFDKNYNLRfM 1932

hCLASP2 DKFGSENVKMIQDSGKVNPKDLDSKYAYIQVTHVIEFFDEKELQERKTEFERSHNIRfM 1770

hCLASP7 ERFGDDVVEIIKDSYPVDKSKLDSKAYIQITYVEYFDYELKDRVTYFDRNYGLRTfL 1851

hCLASP1 DKFGADNVKIIQDSNKNVPKDLDPHYAYIQVTVVTFEEKEIEDRKTDFEMHHNIRfV 1972

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ITAM DOCK motif

hCLASP4 FEAPYTLGKKQGCIEEQCKRRTILTTSNSFFVVKRIPINCEQQINLKPIDGATDEIKD 1859

hCLASP5 YTPFTLEGRPRGELHEQYRRNTVLTTHAFFYIKTRISVIQKEEFVLTPIEVAIEDMK 1870

hCLASP3 YCTPFTLDGRAHGEHEQFKRKTILTTSHAFFYIKTRVNVTHKEEILTPIEVAIEDMQ 1992

hCLASP2 FEMPFTQTGKRQGGVEEQCKRRTILTAIHCFYVVKRIPVMYQHHTILNPIEVAIDEMSK 1830

hCLASP7 FCTPFTPDGRAHGEHEQHKRKTLLSTDHAFYIKTRIRVCHREETVLTPEVAIEDMQ 1911

hCLASP1 FETPFTLSGKKHGGVAEQCKRRTILTTSHLFFVVKRIQVISQSSTELNPIEVAIDEMSR 2032

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Coiled-coil

hCLASP4 KTAELQKLCSSSTDVDMIQQLKLGQWVSQVQVAGPLAYARAFNDSSQASKYPPKKVSELK 1919

hCLASP5 KTLQLAVAINQEPDDAKMLQMVLCQSVGATVNGQPLEVAQVFLAEIPADPKLYRHHNKL 1930

hCLASP3 KTQELAFATHQDPADPKMLQMVLCQSVGTTVNGQPLEVAQVFLSEIPSDPKLFRHHNKL 2052

hCLASP2 KVAELRQLCSSAEVDMIKQLKLGQSVSVQVQVAGPLAYARAFDDTNTKRYPDNKVKLLK 1890

hCLASP7 KTRELAFATEQDPPDAKMLQMVLCQSVGPTVNGQPLEVAQVFLAEIPEDPKLFRHHNKL 1971

hCLASP1 KVSELNQLCTMEEVDMISLQLKLGQSVSVKVNAGPMAYARAFLEETNAKKYPDNQVKLLK 2092

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Coiled-coil

hCLASP4 DMFRKFIQACSIALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIEHQILQEDTMHSP 1979

hCLASP5 LCFKEFIMRCGEAVEKNKRLITADQREYQOELKNYNKLKENLRPMIERKIPELYKPIFR 1990

hCLASP3 LCFKDFTKRCEADALRNKNSLIGPVQKEYQRELGLSSP----- 2090

hCLASP2 EVFRQFVEACGQALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKTS- 1949

hCLASP7 LCFKDFCKKCEADALRNKNSLIGPDQKEYHRELERNYCRREALQPIILTQRLPQLMAPTP- 2030

hCLASP1 EIFRQFADACGQALDVNERLIKEDQLEYQEELRSHYKMDLSELSTVMNEQITGRDDLSKR 2152

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PDZ ligand

hCLASP4 WMSNTLHVFCASGTSSDRGYGSPHYAEV-- 2008

hCLASP5 VESQKRDSFHRSSFRCETQLSQGS----- 2015

hCLASP3 -----

hCLASP2 VLPNSLHIFNAISGTPPTSTMVHGMTSSSSVV 1980

hCLASP7 --PGLRNSLNRASFRKADL----- 2047

hCLASP1 GVDQCTRVISKATPALPTVSISSSAEV-- 2180